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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                               669.5
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/SIDS2/gcgdata/gencseq/gencseqp-embl/AA1995.DAT:*
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AAB62150
AAR70236
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AAW22475
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AAB62148
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P. falciparum Proj
Plasmodium Proj3.
P. falciparum Proj
Plasmodium var-7.
Plasmodium var-7 p
P. falciparum VarC
P. falciparum ECR3
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TNF-R-Pl. vivax Du	701	16	1245	14.6	248.5	ω
CD4-EBA175 fusion	104	14	1786		(J)	N
TNF-R-EBA 175 fusi	010	16	1604	14.7	(J)	1
P. falciparum SABP		21	1435	14.7	(J)	0
ic acid bi	AAW22477	18	1435	14.7	u	9
P. falciparum SABP	AAR70232	16	1435	•	L)	8
parum EB	ABB07656	23	350	•	C)	7
DABP.	AAR70231	16	1061	•	C)	0
vivax PvDBP	ABB07654	23	329	•		5
um falc	AAU76762	23	1501	15.2	58.	4
/ax DABP b	AAY77899	21	1115	•	U	ω
Duffy antigen bind	AAW22478	18	1115	•	(J)	N
Duffy receptor. P	AAR13457	12	1115	•	UΠ	Ľ
odium vi	AAR41044	14	1028	•	O	0
ed an	AAM50533	23	616		$\sigma$	9
falo	AAU76764	23	1421		9	œ
ium	. AAU76761	23	972	•	62.	7
ium DBL	AAY77915	21	311		63.	σ
fal	AAU76760	23	1086		68.	G
:um e	AAY77901	21	749	•	68.	4
Plasmodium ebl-1.	AAW22479	18	749	•		ω
P. falciparum EBL-	AAR70233	16	749	•	68.	N
Ъ	AAW00385	17	1726	•	9	_
	AAW00384	17	2913	•	$\vdash$	0
	AAU76759	23	1143		27.	9
falcip	AAB18352	21	2197	•	42.	8
	AAY77906	21	2182	•	367.5	7
Plasmodium var-1.	AAW22476	18	2182	•	67.	σ
iparum	AAW93944	20	2228	•		5
iparum v	AAB62149	22	351	•	444	4
rum va	6214	22	294		514 .	w
iparum e	7790	21	921	30.5	521	Ν
Plasmodium E31a.	AAW22480	18	921	•	521	

## ALIGNMENTS

AAB62151 RESULT 1 FCR3.varCSA protein; chondroitin sulfate A; CSA; var gene; PFEMP1; erythrocyte membrane protein 1; parasitized red blood cell; PRBC; malaria; protozoacide; ItG2~CS2 DBL2.. 01-SEP-2000; 2000WO-US24195 P. falciparum varCSA polypeptide ItG2-CS2 DBL2 AAB62151 standard; peptide; 308 AA. (USSH ) US DEPT HEALTH & HUMAN SERVICES 01-SEP-1999; 08-MAR-2001. WO200116326-A2 Plasmodium falciparum. 29-MAY-2001 AAB62151; (first entry) 99US-0152023.

Novel FCR3.varCSA protein, useful for modulating parasitized red blood cell binding, sequestration and onset of maternal malaria -

WPI; 2001-235109/24.

Miller LH, Pouvelle B,

Gamain B, Fujii N,

Baruch DI, Smith J;

Buffet Ρ,

Scheidig

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RESULT 2
AAB62150
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           Scherf A,
Gysin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondrolini sulfate A (CSA). The var gene and the corresponding P. falciparum erythrocyte membrane protein 1 (PFEMP1) modulate adhesion of parasitized red blood cell (PRBC) to CSA. The protein and the encoding gene are useful for treating and preventing maternal malaria in a patient identified at a risk for contracting maternal malaria or in a patient afflicted with maternal malaria. The present sequence represents a P. falciparum varCSA polypeptide
                                                                             01-SEP-1999;
                                                                                                     01-SEP-2000;
                                                                                                                                                                                                                                                                                                                            AAB62150
                                                                                                                                 08-MAR-2001
                                                                                                                                                                                                                 malaria;
                                                                                                                                                                                                                                                                                                                                                     AAB62150 standard;
                                                                                                                                                            WO200116326-A2
                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                                                                                                              erythrocyte
                                                                                                                                                                                                                                         FCR3.varCSA protein; chondroitin sulfate A;
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                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCALTNGLSES
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        Miller LH,
Pouvelle B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAKDYEGCKNNKSNNSCYKYCKEYENYITGKKTQYESQEGKFNTEKRQKKPEYNSYSKKD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNDGSNEISGCNPKESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASEYLKDK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKFINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISS
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                                                                                                                                                                                                                              membrane protein 1;
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                                                                                                      2000WO-US24195
                                                                                                                                                                                                                                                                                               (first entry)
                                                                           99US-0152023
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                                                                                                                                                                                                                                                                                                                                                   peptide;
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         Gamain B,
Fujii N,
                                                                                                                                                                                                              rotein 1; parasitized FCR3 var3DBL-gamma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
           Smith
                      Baruch DI,
                                                                                                                                                                                                                           CSA; var gene; PFEMP1;
red blood cell; PRBC;
                       Buffet P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR70236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70236 standard; Protein;
                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                       10-SEP-1993;
                                                                                                                            07-SEP-1994;
                                                                                                                                                                             16-MAR-1995.
                                                                                                                                                                                                                                  WO9507353-A
                                                                                                                                                                                                                                                                                Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                          Erythrocyte binding ligand; Proj3; binding domain; malaria; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel FCR3.varCSA protein, useful for modulating parasitized cell binding, sequestration and onset of maternal malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1995
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172; Conserv
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Pred. No. 2.6e-72;
8; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic studies of the chloroquine resistance locus. The 4 genes, EBL-e1 (AAQ83526), E31a (AAQ83527), EBL-e2 (AAQ83528) and Proj3 (AAQ83529), encode the proteins given in AAR70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, mammallan, insect, and in vaccinia virus and adenovirus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erythrocyte binding ligand (EBL) family genes were cloned from P. falciparum chromosome 7 subsegment libraries constructed during genetic studies of the chloroquine resistance locus. The 4 genes, EBL-el (AAQ83526), E3la (AAQ83527), EBL-e2 (AAQ83528) and Proj3
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                                                                                                                                                                                                                                              DBL gene family; SABP; sialic acid binding protein; vaccine; therapy; Duffy binding like gene; Duffy antigen binding protein; erythrocyte; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitnis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22482 standard;
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DB; AAQ83529.
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Pred. No. 8.9e-51;
4; Mismatches 109;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents Proj3 of Plasmodium. Proj3 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see ANT/2889 and ANT/2888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 50-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid
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                                                                                                                                                                                   LTNGLSESE-KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKL
                                                                                                                                                                                                                       ISKKQ--NDVAKA-KDKIGKFFSKDGSKSPSGLSR-----QEWWKTNGPEIWKGMLCA
                                                                                                                                                                                                                                                            ISSCRYIKDTSQTIKSKLG-----DQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA
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                                                                     ENIIKDACNEINSTQQC--NDAKHRCNQACRAYQEYVENKKKEFSGQTNNFVLKANVQPQ
                                                                                                                                                LTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAERQKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 669.5; DB 18; Pred. No. 8.9e-51; 54; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to ebl-1 polypeptides that are encoded by the DBL (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the culture supernatant after crythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and Sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated protein binding domains from Plasmodium vivax and Plasmodium falciparum erythrocyte binding proteins useful for vaccinating against
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                                          ENTIKDACNEINSTOOC--NDAKHRCNOACRAYQEYVENKKKEFSGOINNFVLKANVOPO
                                                                                                                                                                                                                      LTNGLSESE-KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKL
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                                                                                                  EDKVEDVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKF--NTEKRQK
                                                                                                                                                            LTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAERQKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 669.5; DB 21; Pred. No. 8.9e-51;
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SABP; malaria; vaccine; immunisation;
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GKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHESQTENIKTDD 1415 GNDGSNEISGCNPKESYPDWDCKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPE 57 Matches Query Match Best Local

Local Similarity les 133; Conser

Conservative

39.2%;

Score 669.5; DB 1 Pred. No. 1.1e-50; 4; Mismatches 109

109; 18;

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RESULT 6
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                                                                                               the Duffy binding like (DBL) family of genes which have homology to the COLING protein (DABP) and sialic acid binding protein (SABP) conserved regions (see AAT72889 and AAT72888 respectively). The conserved regions of the cytoadherence and antigenic variation of the cytoadherence and antigenic variation of the cytoadherence and antigenic variation of the cytoadherence and schizonts to the erythrocyte supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the cytoadherence. This sequence can be used in the compositions of the parasite. This sequence can be used in the compositions of the constraint, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP.
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                             The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially plasmodium falciparum or Plasmodium vivax).
Sequence
                                                                                                                                                                                                                                                                                                                                                     This sequence represents var-7 the Duffy binding like (DBL) for
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 61-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitnis
                                                                                                                                                                                                                                                                                                                                                                                                                                             binding proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBL gene family; SABP; sialic acid binding protein; vaccine; therapy, Duffy binding like gene; Duffy antigen binding protein; erythrocyte; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wellems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium vivax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1646 DPEYKGYEYKDGVQPIQGNEYLLQK 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,
TE;
3060 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller
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                                                                                                                                                                                                                                                                                                                                                                 of Plasmodium. Var-7 belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DS,
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SXXCCCCCCCCCCCCXXX PFFXX DR
                                            The invention relates to ebl-1 polypeptides that are encoded by the DBL (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the culture supernatant after crythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and sialic acid receptors on crythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against malaria. The present sequence represents the var-7 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DBL gene; Duffy-binding like gene; ebl-1; Duffy Antigen Binding Protein; DABP; Sialic Acid Binding Protein; SABP; malaria; vaccine; immunisation; protozoacide; var-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Columns 109-124; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated protein binding domains from plasmodium vivax and plasmodium falciparum erythrocyte binding proteins useful for vaccinating agains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1999
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DB; AAZ98287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitmis C,
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        The invention relates to a P. falciparum FCR3 varCSA protein, that is capable of binding to chondroitin sulfate A (CSA). The var gene and to corresponding P. falciparum erythrocyte membrane protein 1 (PFEMPI) modulate adhesion of parasitized red blood cell (PRBC) to CSA. The protein and the encoding gene are useful for treating and preventing maternal malaria in a patient identified at a risk for contracting maternal malaria or in a patient afflicted with maternal malaria. The
                                                                                                                                                                                                       Scherf A,
                                                                                                                                                                                                                                                                              01-SEP-2000;
                                                                                                                                                                                                                                                                                                                               WO200116326-A2
                                                                                                                                                                                                                                                                                                                                                                             malaria; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                          FCR3.varCSA protein; chondroitin sulfate A; CSA; var gene; PFEMP1 erythrocyte membrane protein 1; parasitized red blood cell; PRBC;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ρ.
                                                                                                          Disclosure;
                                                                                                                                                                                           Gysin
                                                                                                                                                                                                                                                        01-SEP-1999;
                                                                                                                                                                                                                                                                                                       08-MAR-2001
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                                                                                                                                FCR3.varCSA protein, ubinding, sequestration
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                                                                                                                                                                                           Pouvelle
                                                                                                                                                                                                        Miller LH,
                                                                                                                                                                                                                               DEPT
                                                                                                        Page 72-73; 78pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%;
                                                                                                                                                                                           Gamain B,
Fujii N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- ASEYLKDK
                                                                                                                                                                                                                                Ŗ٦
                                                                                                                                                                                                                                                                                                                                                                              A4 DBL4-gamma
                                                                                                                                                                                                                                HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                useful for
n and onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 669.5;
Pred. No. 1.
 Ъ.
                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
falciparum varCSA polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                             A4 DBL4-gamma
                                                                                                                                                                                             Smith
                                                                                                                                                                                                        Baruch DI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308
                                                                                                                                modulating pof maternal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109;
                                                                                                                                                                                                         Buffet
                                                                                                                                                                                                                                                                                                                                                                                                      var gene; PFEMP1;
                                                                                                                                parasitized
l malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                         ۵,
                                                                                                                                                                                                        Scheidig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3060
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                                                                                                                                              plood
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Best Local
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The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondroitin sulfate A (CSA). The var gene and the corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1)
                                                                                                                                Scherf Å,
Gysin J,
                                             Claim 12; Page 63-71;
                                                                                                  WPI; 2001-235109/24.
N-PSDB; AAF57301.
                                                                                                                                                                                     01-SEP-1999;
                                                                                                                                                                                                         01-SEP-2000;
                                                                                                                                                                                                                              08-MAR-2001
                                                                                                                                                                                                                                                  WO200116326-A2
                                                                                                                                                                                                                                                                        Plasmodium
                                                                                                                                                                                                                                                                                                    FCR3.varCSA protein; chondroitin sulfate A; erythrocyte membrane protein 1; parasitized
                                                                                                                                                                                                                                                                                                                                    P. falciparum FCR3.varCSA protein
                                                                                                                                                                                                                                                                                                                                                            29-MAY-2001
                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                 AAB62142;
                                                                                                                                                                                                                                                                                                                                                                                                   AAB62142 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A4
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                                                                binding,
                                                                FCR3.varCSA protein, useful for binding, sequestration and onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
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                                                                                                                                                                                                                                                                                            protozoacide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYEQQTAKFDKDKKDKKFDGTSAEVDVAAVSSVHEYLQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYESQEGKFNTEKRQKK-----PEYNSYSKKDASEYLKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDYGPDIWKGMYCGLSHHIKNGNKEQLRKNLTDNNKYTKISSK-----LEDFASRPQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATT--EKGDTHIDDNKKLQEWW 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWFIEWGDQFCRERVVKINQLKTGC----NEYECGSQENGKKEACKNACEAYKSWLKDWKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWYVEWSDEFCRERKKLEDKVEDVCIKAKDYE-GCKNNKSNNSCVKVCKEYENYITGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIHGPKIWEGMLCALT----NGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QMFYTYGDYRDFLFGTDISK-----GHGKESALGKKIDSLFKNGDQKSPSGKTPTEWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETELRKAFIECAAIETFWLWDKYKEDKKDEKKTEGGGISDDPDDPQKKLEGGTIPEDFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEDILTKFINCAAKETHFAWHKYKKDNV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNDGSNEISGCN-----PKESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRK
                                                                                                                               Miller LH,
Pouvelle B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQDGTKKIEECNTKYYPTKNDYPGWNCTDKVINREEGSCMPPRRQKLCIHNLEHLSEKAT
                                                                                                                                                                                                                                                                      falciparum.
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                                                                                                                                                                                                        2000WO-US24195
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                   99US-0152023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                                           78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
                                                                                                                               Gamain B,
Fujii N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                           English
                                                                                                                                                                                                                                                                                                                                                                                                    3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 600; DB 22;
Pred. No. 1.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                              Baruch DI,
Smith J;
                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                               modulating parasitized of maternal malaria -
                                                                                                                                                                                                                                                                                                   CSA; var g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·----NAENELKSGKIPEGFRK
                                                                                                                                        Buffet
                                                                                                                                                                                                                                                                                                              var gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308
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                                                                                                                                                                                                                                                                                                     cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407;
                                                                                                                                      Scheidig C;
                                                                                                                                                                                                                                                                                                               PFEMP1;
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                                                                           red
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                                                                           blood
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Best Local
                                                                                                    Chitnis
Wellems
                    New erythrocyte binding domain polypeptide(s) - Plasmodium binding proteins, used in diagnosis, prevention of malaria
Disclosure;
                                                                   N-PSDB;
                                                                             WPI; 1995-123427/16.
                                                                                                                                                                                 07-SEP-1994;
                                                                                                                                                                                                                               WO9507353-A.
                                                                                                                                                                                                                                                                                      Erythrocyte
                                                                                                                                                                                                                                                                                                             P. falciparum
                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                            10-SEP-1993;
                                                                                                                                                                                                        16-MAR-1995
                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                             AAR70234;
                                                                                                                                                                                                                                                                                                                                                                                AAR70234 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulate adhesion of parasitized red blood cell (PRBC) to CSA. The protein and the encoding gene are useful for treating and preventing maternal malaria in a patient identified at a risk for contracting maternal malaria or in a patient afflicted with maternal malaria. The present sequence represents the P. falciparum FCR3.varCSA protein.
                                                                                                                                                                                                                                                                                                                                      22-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 ALTNGLS-ESEKKNILODYSYNKLNNAEKDDCCLEKFASKPOFLRWYVEWSDEFCRERKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TDISSCRYİKDTSQTİKSKLGDQATTEKGDTHIDDNKKLQE----WWTİHGPKİWEGMLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
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                                                                                                    TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DGSNEISGCNPKE--SYPDWDC--KKNIDNSHSGACMPPRRQKLCVRD---LTQGGEIRK
                                                                   AAQ83527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLLKLEAGC---KEYE-CNGSNDGKTQECAEACVTYQNFIKKWKTEYERQREKFKKDKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDKVEDVCIKAKDYEGC - - KNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        KK--YKDYPSTERDIEKATCAHEYLNMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKPEYNSY--SKKD-----ASEYLKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDISNDKKIITVTNSVTTILNENNKKKQ------DKKKDEELRKIFWEKNKKFIWEGMIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSRGGIEGCNPKTYGQYPKWGCIYGKSKEN-ENGICMPPRRKKLCINNIQYLNYETENKR
                                                                                                               Miller LH,
                                                                                                                                                                                                                                                                                    binding ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3542 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                               E31a.
                                                                                                                                                           93US-0119677
                                                                                                                                                                                 94WO-US10230
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                                                                                                             Peterson
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                                                                                                                                                                                                                                                                                    E31a; binding
                                                                                                                                                                                                                                                                                                                                                                                 793
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Pred. No. 8e-42;
""smatches 105;
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                                                                                                              DS,
                                                                                                           Sim
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                                                                                                                                                                                                                                                                                   domain; malaria; therapy;
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                              isolated f
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Page

51-52;

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English

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RESULT 11
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Best Local S
Matches 127
WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DBL gene family; SABP; sialic acid binding protein; vaccine; Duffy binding like gene; Duffy antigen binding protein; eryt; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAQ83529), encode the proteins given in AAR70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, mammalian, insect, and in vaccinia virus and adenovirus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erythrocyte binding ligand (EBL) family genes were cloned from P. falciparum chromosome 7 subsegment libraries constructed during genetic studies of the chloroquine resistance locus. The 4 genes, EBL-el (AAQ83526), E3la (AAQ83527), EBL-el (AAQ83528) and Proj
                                                                                                                                                                                                                                                                                                                                                                                                           W09640766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium E31a.
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                                                                                    Wellems
                                                                                                               Chitnis
                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                     07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
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1997-052231/05
DB; AAT72895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682 NYKKQKGRYTEVKKIPLYKEDKDVKNSDDARDYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV----CKEYENVITGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD------NKKLQEWWTIHG
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                                                                                    TE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-----FINCAAKETHFAWHKYKKD-NVNAEN---ELKSGKIPEGFRKQMYYTFGDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVIWEGMLCALSYDTSLNNVNPETHKKLTEGNNNFEKVIFGSDSSTTLSKFSERPQFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKIWEGMLCALTNGLS -----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DICLGTDISS---KKDTSKGV-----GKVKCNIDDVFYKISNSIRYRKSWWETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGRTTYGECYRKETYSEWTCDESKIKMGQHGACIPPRRQKLCLHYL--
                                                                                                                                                                     DEPT HEALTH & HUMAN SERVICES
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                                                                                                               Miller LH,
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                                                                                                                                                                                                                               95US-0487826
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                                                                                                               Peterson DS,
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Pred. No. 4.2e-38;
6; Mismatches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
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RESULT 12
AAY77902
ID AAY77
XX

AAY77902 standard;

Protein;

921

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OS XWW XXX AC

P. falciparum ebl-1 related

polypeptide.

ebl-1; Duffy Antigen Binding Protein; SABP; malaria; vaccine; immunisation;

13-JUN-2000 AAY77902

(first entry)

DBL gene; Duffy-binding like gene; DABP; Sialic Acid Binding Protein; protozoacide.

Plasmodium falciparum

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Вb
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Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially Plasmodium falciparum or Plasmodium vivax).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see ANT72889 and ANT72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid binding proteins
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                                                                                                                                                                                                                                                                                   518
                                                                                                                                                                                        565
                                            274 QYESQEGKFNTEKR--QKKPEYNSYSKKDASEYLK 306
                                                                                                                                         217 YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT
                                                                                                                                                                                                                                                                                                                                                                           458 NTNELKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYTFADYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 NGRTTVGECYRKETYSEWTCDESKIKMGQHGACIPPRRQKLCLHYL-----EKIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DGSNEISGCNPKESYPDWDC-KKNIDNSHSGACMPPRROKLCVRDLTQGGEIRKPEDILT
NYKKQKGRYTEVKKIPLYKEDKDVKNSDDARDYLK
                                                                                          LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID
                                                                                                                                                                                     PVIWEGMLCALSYDTSLNNVNPETHKKLTEGNNNFEKVIFGSDSSTTLSKFSERPQFLRW
                                                                                                                                                                                                                   PKIWEGMLCALTNGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW
                                                                                                                                                                                                                                                                                   DICLGTDISS---KKDTSKGV-----GKVKCNIDDVFYKISNSIRYRKSWWETNG
                                                                                                                                                                                                                                                                                                              DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD-----NKKLQEWWTIHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 521; ·DB 18;
Pred. No. 5.2e-38;
6; Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 921;
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R29DBL2-gamma

R29DBL2-gamma

CSA; red k

; var gene; PFEMP1; blood cell; PRBC;

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RESULT 13
AAB62147
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Matches
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                                             AAB62147
 29-MAY-2001
                       AAB62147;
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to ebl-1 polypeptides that are encoded by the DBL (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the culture supernatant after erythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Columns 61-66; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated protein binding domains from Plasmodium vivax and Plasmodium falciparum erythrocyte binding proteins useful for vaccinating against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim KL,
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                                                                                                                                                                                                        PKIWEGMLCALINGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW
                                                                                                                                         LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID
                                                                                                                                                    YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT
                                                                                                                                                                                                                                             DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD------NKKLQEWWTIHG
                                                                                                                                                                                                                                                                           NTNELKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYTFADYR
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                                            standard;
                                                                                                 NYKKOKGRYTEVKKIPLYKEDKDVKNSDDARDYLK
                                                                                                                                                                                                                                    DICLGTDISS - - - KKDTSKGV - - - -
                                                                                                                     QYESQEGKFNTEKR--QKKPEYNSYSKKDASEYLK 306
                                                                                                                                                                                    PVIWEGMLCALSYDTSLNNVNPETHKKLTEGNNNFEKVIFGSDSSTTLSKFSERPQFLRW
                                                                                                                                                                                                                                                                                         K-----FINCAAKETHFAWHKYKKD-NVNAEN---ELKSGKIPEGFRKQMYYTFGDFR 110
                                                                                                                                                                                                                                                                                                                      NGRTTVGECYRKETYSEWTCDESKIKMGOHGACIPPRRQKLCLHYL---
                                                                                                                                                                                                                                                                                                                                          DGSNEISGCNPKESYPDWDC-KKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDILT
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(first entry)
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                                            peptide;
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                                                                                                                                                                                                                                                                                                                                                                             Score 521; DB 21;
Pred. No. 5.2e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scherf A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malaria; protozoacide;
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29-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondroitin sulfate A (CSA). The var gene and the corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 FIKCAAKETNLLWDKYKNDKNEAEELLKKGKIPEDFMRIMFYTFGDFRDFCLENDMG---
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                                                                                          standard;
                                                                                                                                                                                                STC---KSIDG-GQLKCDRGCNNKCDEYKKYMRKKKEEWNLQD-KYYKDKRENK
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(first entry)
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                                                                                          peptide;
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Pred. No. 4.7e-38;
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Gysin J,
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            AAW93944 standard;
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A4tresDBL3-gamma.
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                                                                                                                                                                                                                                                        DTSQTIKSKLGDQATTEKGDTHIDDNKKLQE---WWTIHGPKIWEGMLCALTNGLSESEK
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                                                                                                                                                         KVEDVCIK--AKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKF---
                                                                                                                                                                                                                                           DVT-TAKKKI--TAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCALSYN-TETKK
                                                                                                                                                                                                                                                                                              SAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISEKIADH
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                                                                               NNGLAVKEANSETYKNDPEVTEANSAKHARDYLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 AA;
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            protein;
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Fujii N,
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              2228
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Pred. No. 1.2e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                           131;
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red blood cell; PRBC;
                                                                               340
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                         invention are capable of acting as receptors for malaria antigens present on the surfaces of malaria infected erythrocytes, by binding to these antigens the carbohydrates prevent rosette formation by the blood cells, this prevents occlusion of capillaries as is seen in cerebrial malaria caused by Plasmodium falciparum. The products of the invention can be used to treat malaria or to vaccinate against it, or used to design a model to identify compounds that bind to PTEMPI. The carbohydrates, polypeptides and antibodies of the invention can be used as a medicament for dissolving the rosettes formed by erythrocytes infected by a malaria parasite. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel Plasmodium falciparum erythrocyte membrane protein (EMP), PfEMP1, which is capable of binding to a carbohydrate which exhibits at least one negatively charged glycosamino-glycan (GAG)-like moiety and has antiaggregational, antiocclusional and antimalarial activity. The carbohydrates of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen receptor; in
capillary occlusion;
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glycosamino-glycan-like moiety; antiaggregational; antimalarial;
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                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                      Similarity
                                            EKMNKYKEIKNERKCSTERSAPNLVSHPQTWWENNGKYIWHGMVCALTSKDKIAKGVEKK 1155
                                                                                                                    PDSKEALLKAFVESAAIETFFLWHRYKEEKKAVAQEGAGHGLPRVEEGSPEYDPEDKLKE
                                                                                                                                                                                   WRCVTPSGEPTTSSDKNGAICVPPRRRRLYIKKIVDWATKTESPQASGSEASSTSGSTTP
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on; cerebral malaria; treatment; vaccine;
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Pred. No. 2.6e-25;
9; Mismatches 123;
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	Search completed: June 20, 2003, 15:02:56 Job time : 50.5417 secs	arch comp b time :	Se
	1336 KFLE 1339	13	ф
	303 EYLK 306	ω	Qy
1335	1276 NCPGCGKHCSSYRKWIERKKIEFHKQSNAYGQQKTDATRNNGNTFDKEFCKTLETWPDAA 1335	12	DЪ
302	256SCVKVCKEYENYITGKKTQYESQEGKFNTEKRQ-KKPEYNSYSKKDAS 302	2	Qy
1275	1216 PTYFRWFEEWGESFCRERKKRLKQIKVDCKVENGDVGRCSGDGEACDSISTHDYSTVPSF 1275	12	D.
255	211 PQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNN 255	2	VΩ
1215	1156 PQKIENPENLWDEANKKPKPPQYQYTNVKLDENSGTSPRTTQTQASSDNTPTTLTHFVKR 1215	11	Дb

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Sequence:
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2: | /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
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US-08-487-826B-29
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US-08-568-459A-21

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538.603 Million cell updates/sec
Sequence 4, Appli
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Sequence 29, Appl
Sequence 29, Appl
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Sequence 12, Appl
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US-08-568-459A-12
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109	112	112	112	119.5	119.5	119.5	127.5	127.5	127.5	135	135	. 135	156	156	156	178	178
6.4	6.6	6.6	ი ი	7.0	7.0	7.0	7.5	7.5	7.5	7.9	7.9	7.9	9.1	9.1	9.1	10.4	10.4
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Sequence 2, Appli	Sequence 19, Appl	•	•	Sequence 18, Appl	•	18,	Sequence 16, Appl	`	-	•	•	-	Sequence 15, Appl		Sequence 15, Appl	Patent No. 5198347	Patent No. 5198347

## ALIGNMENTS

Sequence 12, Patent No. !

Application US/08568459A 5849306

GENERAL INFORMATION:

APPLICANT: APPLICANT:

Sim, Kim...
Chitnis, Chetan
Chitnis, Chetan
Miller, Louis H.
Meterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
Wellems, Thomas E.
Wellems, BINDING DOMAINS FROM PLASMODIUM VIVAX
TOTAL FALCIPARUM ERVTHROCYTE

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE NUMBER OF SEQUENCES: 37

BINDING PROTEINS

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US-08-568-459A-12
Query Match
                                                                                                                                                          TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEO ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 07-DEC-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
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STATE: California
                                                 ORGANISM:
                                                                                                                   TOPOLOGY:
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                                                Plasmodium falciparum
                                                                                                                   linear
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16th Floor
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Length 2710;
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US-08-487-826B-12
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                                                                                                     TELEFAX: (619) 235-0176
NFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
      HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chitnis, Cneta...
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                        TOPOLOGY:
                                                    STRANDEDNESS:
                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                         CLASSIFICATION:
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Newport Beach
California
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                                                                                       2710 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative.
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                                        linear
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O Newbort Center Drive 16th Floor
                                                                                                                                                     (619) 235-8550
                                                                                                                                                                                                                                                          10-SEP-1993
N: 435
                    protein
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; ORGANISM: Pla
US-08-487-826B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
             TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: PatentT
                                                                                                             NAME: Fuller, Michael REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 92660
                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1646 DPEYKGYEYKDGVQPIQGNEYLLQK 1670
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                                                                                                                                                                                                                                                                                                                                                Newport Beach
California
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                                                                                                                                                                                                                                                                                                                                                                                    620 Newport
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Su, Xin-zhaun
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Miller, Louis H.
                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                PatentIn
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amino acids
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                                                                                                                                                                                                                                Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  David S
                                                                                                                                                                                               US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                                    Center Drive
                                                                                                            36,516
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                                                                                               NIH121.1FWDV1
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Pred. No. 6.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                Version
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16th Floor
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                                                                                                                                                                                                                                #1.25
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US-09-210-288-12
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US-08-487-826B-14
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wellems, III.

TITLE OF INVENTION: BINDING DOMAINS FROM FLICTIFIED OF INVENTION: AND PLASMODIUM FALCIPARUM

TITLE OF SPOHENCES: 45
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                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                              COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
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TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: si
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                                 NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                       APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                        STREET:
                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                     T: 620 Newport Center Drive
Newport Beach
                                                                                                                                                                                                                                                                  92660 '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTNGLSESE-KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHESQTENIKTDD 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILTKFINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENIIKDACNEINSTQQC---NDAKHRCNQACRAYQEYVENKKKEFSGQTNNFVLKANVQPQ 1645
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                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                   Wellems, Thomas E.
Wellems, Thomas E.
VENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Su, Xin-zhaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sim, Kim L.
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                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                        Knobbe Martens Olson & Bear
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                                   29,655
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Pred. No. 6.7e
54; Mismatches
                   NIH121.001CP1
                                                                                                                                                                  Version
                                                                                                                                                                                                                                                                                                                                        16th Floor
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RESULT 5
US-08-568-459A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/568,459
FILING DATE: 07-DEC-1995
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thoma
                                                                                                                                                                                                         COUNTRY: U
ZIP: 92660
                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 39.2%; ocal Similarity 40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1644 DPEYKGYEYKDGVQPIQGNEYLLQK 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 LTNGLSESE-KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKL 231
|} ::::: |: | |||||:|: : ||:||:|||||| :|| :|| ||:|
1526 LTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAERQKK 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 DILTKFINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GNDGSNEISGCNPKESYPDWDCKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Application US/08568459A
5849306 ·
                                                                                                                                                                                                                                                        Newport Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKKQ--NDVAKA-KDKIGKFFSKDGSKSPSGLSR-----QEWWKTNGPEIWKGMLCA
         Israelsen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDKVEDVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKF--NTEKRQK 289
                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                   Chitnis, Cuc.
Miller, Louis H.
Forson, David S.
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                                                                                                                                                                                                                                                                                            Knobbe Martens Olson &
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                                                  07-DEC-1995
N: 435
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                                                                                                                                                                                                                                                                                                                             AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                               Thomas E.
                                                                                   US/08/568,459A
                                                                                                                                                                                                                                                                          Center Drive
29,655
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Pred. No. 7.9e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308
                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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US-08-487-826B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 235-0176
NFORMATION FOR SEQ ID NO: 8:
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                PPLICANT:
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                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    COUNTRY: UZIP: 92660
                                                                                                                                                                                                                                                                                                                                             it No.
 APPLICATION NUMBER:
                                                                                                                                 STATE:
                                                                                                                                                          STREET:
                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Plasmodium falciparum
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LECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                              682 NYKKOKGRYTEVKKIPLYKEDKDVKNSDDARDYLK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 PKIWEGMLCALTNGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD------NKKLQEWWTIHG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565 PVIWEGMLCALSYDTSLNNVNPETHKKLTEGNNNFEKVIFGSDSSTTLSKFSERPQFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 DICLGTDISS---KKDTSKGV------GKVKCNIDDVFYKISNSIRYRKSWWETNG
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>. 5993827
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127; Conservative
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                                                                                                                                            Newport Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYESQEGKENTEKR--QKKPEYNSYSKKDASEYLK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                               California
                                                                                                                                                       620 Newport Center Drive
                                                                                                                                                                                                                                                                                    Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
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                         PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                        Peterson,
                                                                                                                                                                                                                                          Su, Xin-zhaun
Wellems, Thomas E.
                                                                                                                                                                      Knobbe Martens Olson & Bear
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                                                                                                                                                                                                   BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
45
                                                                                                                                                                                                                                                                        David S.
US/08/487,826E
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Pred. No. 8.7e-40;
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                                                                                                                                                        16th Floor
                          #1.25
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Best Local
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                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                       APPLICANT:
                    COUNTRY: US
                                                  STATE:
                                                                             STREET:
                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                          625
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Patent No. 6392026
GENERAL INFORMATI
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 8:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                 APPLICANT: Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE: ORGANISM: Pla
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HYPOTHETICAL: NO
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STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 NYKKOKGRYTEVKKIPLYKEDKDVKNSDDARDYLK 716
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                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DGSNEISGCNPKESYPDWDC-KKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDILT 61
                                                                                                      Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKIWEGMLCALINGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGRTTVGECYRKETYSEWTCDESKIKMGQHGACIPPRRQKLCLHYL--
                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD-----NKKLQEWWTIHG
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                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09210288
                                                                                                                                                                                                                                                                        Chitnis, Cue...
Miller, Louis H.
                                                                                                                     E: Knobbe Martens Olson & 620 Newport Center Drive
                                                                   S
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N: 435
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Pred. No. 8.7e-40;
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                                                                                                                         16th Floor
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                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Plasmodium falciparum US-09-210-288-8
                                                                                                                                                                                                                                                                                       US-08-487-826B-16
                                                                                                                                                                                                                              Sequence 16, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 235-01: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Fuller, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                  NUMBER OF SEQUENCES: 4
                                                                                   APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/210,288
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                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                          274 QYESQEGKFNTEKR--QKKPEYNSYSKKDASEYLK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 NTNELKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYTFADYR 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD-----NKKLQEWWTIHG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K------FINCAAKETHFAWHKYKKD-NVNAEN---ELKSGKIPEGFRKQMYYTFGDFR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGRTTVGECYRKETYSEWTCDESKIKMGQHGACIPPRRQKLCLHYL---
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                                                                                                                                                                                                                                                                                                                                                                                                                            LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKIWEGMLCALTNGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DICLGTDISS----KKDTSKGV-------GKVKCNIDDVFYKISNSIRYRKSWWETNG
E: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th
ewport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          921 amino acids
                                                                                                                                                                         Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                        Sim, Kim L.
                                                                                                                                          Su, Xin-zhaun
                                                                                                                                                          Peterson, David S.
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SYSTEM: PC-DOS/MS-DOS
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) 235-0176
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Pred. No. 8.7e-40;
6; Mismatches 106
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                  16th Floor
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Best Local :
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ANTI-SENSE: NO
FRAGMENT TYPE:
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LENGTH: 2182 amino acids
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TELEFAX: (619) 235-0176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                              1114
                                                                                                                                                                                                                                                                                                     1054 ASGSTEQEKEKMKQIQAKIKKILNGATSGVPPVTKNSVKTPQQTWWENIAKDIWNAMVCA 1113
1294
                                                                         1234 YNVLQDLSSSCAKPCRLYKTWIEKKKTEYEKQQKAYEQQKSNYENEQKDKCQTQSNNNAN
                                                                                                                                                  1174 TLKNFVEIPTFFRWLHEWGNSFCFERAKRLAQIKHECMDEDGEKQYSGDGEYCEEIFSKQ 1233
                                   303
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                                                                                                                                                                                                                                                                                                                                                                                 994 DPQTQLQQTGVIPPDFLRQMFYTLADYKDILYSGSNDTSDTTGKQTPSSSNDNLKNIVLE 105:
                                                                                                                                                                                                                                                                                                                                             142 EKGDTHIDDNK----
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                                                                                                                                                                          CLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIK---AKDYEG----CKNNKS--
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EF 1295
                                   EY . 304
                                                                                                                                                                                                                              LTYKENDARGTSAKIEQNKDLKKALWDEANKNTPIEKYQYTNVKLEDESGAKSNDTIQPP 1173
                                                                                                                                                                                                                                                                  LT----NGLS-----
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.7e-25;
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WESULT 9 US-08-568-459A-6 ; Sequence 6, Application US/08568459A ; Patent No. 5849306

GENERAL INFORMATION:

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US-08-568-459A-6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: pi
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94000
COMPUTER READABLE FORM:
MENTIM TYPE: Floppy disk
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NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 352
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                                                                                                                                                173 LTNGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLE 232
                                                                                                                                                                                         209
                                                                                                                                                                                                             116 TDI---SSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA 172
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                                                                                    DKVEDVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPE 292
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                          YNSYSK-KDASEYLKDK 308
NNLYNKFEDSKAYLRSE
                                                      KQLEKIC----ENKNCSEKK----CKNACSSYEKWIKERKNEYNLQSKKFDSDKKLNK-K 351
                                                                                                                                                                                    LDVWRDINTNKLSEKFQKIFMGGGNSRKKQ-----
                                                                                                                                                                                                                                                                           EDILTKFINCAAKETHFAWH-KYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFG 115
                                                                                                                                                                                                                                                                                                          SSVFGCKTKISKVKKKWNCYSNNKVTKPEGVCGPPRRQQLCLGYIFLIRDGNEEG----- 163
                                                                                                                                                                                                                                                                                                                                        NEISGCNPKES~ YPDWDC-KKNIDNSHSGACMPPRRQKLC-----VRDLTQGGEIRKP
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California
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Miller, Louis H.
Miller, Louis H.
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                                                                                                                          ----KHIPKGKTCKRHNNFEK-----
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26.8%;
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BINDING DOMAINS
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368
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Pred. No. 1.6e-16;
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FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                    ---IPQFLRWLKEWGDEFCEEMGTEV 300
                                                                                                                                                                                                                                                                                                                                                                              116;
                                                                                                                                                                                 -NDNNERNKWWEKQRNLIWSSMV-- 260
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US-08-487-826B-6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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ORGANISM: Pla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                           233 DKVEDVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPE 292
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                                                                                                                                                                                   164 ---LKDHINKAA--NYEAMHLKEKYENAGGDKICNA-----ILGSYADIGDIVRG
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                                                                                         LTNGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLE
                                                                                                                         LDVWRDINTNKLSEKFQKIFMGGGNSRKKQ-----NDNNERNKWWEKQRNLIWSSMV--
                                                                                                                                                      TDI----SSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA 172
                                                                                                                                                                                                        EDILTKFINCAAKETHFAWH-KYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFG
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Miller, Louis H.
Peterson, David S.
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(619) 235-0176
R SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
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-ENKNCSEKK-----CKNACSSYEKWIKERKNEYNLQSKKFDSDKKLNK-K 351
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS: 45
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; Pred. No. 1.6e-16;
45; Mismatches 116;
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                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                    164 ---LKDHINKAA--NYEAMHLKEKYENAGGDKICNA-----ILGSYADIGDIVRG
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                               LTNGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLE, 232
                                                                 LDVWRDINTNKLSEKFQKIFMGGGNSRKKQ-----NDNNERNKWWEKQRNLIWSSMV--
                                                                                                   TDI---:SSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA. 172
                                                                                                                                                                  EDILTKFINCAAKETHFAWH-KYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFG 115
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SYSTEM: PC-DOS/MS-DOS
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- NO: 6:
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26.8%;
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Pred. No. 1.6e-16;
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16th Floor
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-IPQFLRWLKEWGDEFCEEMGTEV 300
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US-08-568-459A-21
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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NAME: Israelsen, Ned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                        Local Similarity
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139 ATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCAL-TNGLSESEKKNILQDYSYNKLNNA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                        12
                                                                     79 KKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQ 138
                                                                                                                                      22 CKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKY 78
                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                     XXXXXXXXXXXXXXXXQFLRSMMYTFGDYRDICLNTDIS-----KKQNDVXXXXXXXX 126
                                                                                                      Application US/08568459A
                                                                                                                                                                                                                                                                                                                                                                                         311 amino acids
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Chitnis, Chetan
Miller, Louis H.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      Score 263.5; DB 2
Pred. No. 1.4e-16;
19; Mismatches 158
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                                                                                                                                                                                                        Length 311;
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US-08-487-826B-33
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                                                                                                              Matches
                                                                                                                                        Query Match
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                                                                                                                           Best Local Similarity
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
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    72
                          79 KKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQ 138
                                                     22 CKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKY 78
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T. 620 Newport Center Drive 16th Floor
Newport Beach
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Miller, Louis H.
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                        15.4%; 26.3%;
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                                                                                                                        Score 263.5; DB 2
Pred. No. 1.4e-16;
                                                                                                              Mismatches
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                                                                                                                                        DB 2;
                                                                                                              158;
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RESULT 14
US-09-210-288-21
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Best Local S
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HYPOTHETICAL: NO
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
                                                                                                                                                                                                                                         MOLECULE TYPE:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Newport Beach
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                              CKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKY 78
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Miller, Louis H
                                                                                              Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
37
                                                                                            15.4%; Score 263.5; DB 4; 26.3%; Pred. No. 1.4e-16; tive 19; Mismatches 158;
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. 14;	Gaps	15; 104;	Length 1115 Indels 1	3 2; e-15; 127;	ore 259; DB ed. No. 2.1e Mismatches	Score Pred. 38; Mis	15.2%; / 24.9%; cvative	h Similarity 89; Conserva	:ch 11 Simi 89;	Query Match Best Local Matches 8	<b>7</b> m O
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					.001CP1	NIH121.001CP1	NUMBER: NI INFORMATION:		REFERENCE/DOCKES TELECOMMUNICATION	REFE TELECO	
						1	d I	_	ATTORNEY/AGENT NAME: Israe	ATTORNE :	٠.
					;		50	FILING DATE: 07-DE CLASSIFICATION: 43	FILING DATE: 0 CLASSIFICATION:	FILI	
							ÀT	APPLICATION DATA: CATION NUMBER: US		CURRENT	
				n #1.25	Version	/MS-DOS se #1.0,	YSTEM: PC-DOS/M PatentIn Release	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0	OPERATING SOFTWARE:	OPER	
							Floppy disk	TYPE: Flop	UM TYPE:	MEDIUM	
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							- 101	California		STATE:	
	•			Floor	16th	er Drive	rt Center	20 Ne	0	STREET:	
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		•			1	, E	Thon	Wellems,	ANT:	APPLICANT:	
						s.	Davi	erson		APPLICANT:	
							Chetan Louis H	Chitnis, Miller,		APPLICANT:	
								INFORMATION: ANT: Sim, Kim	₹.5	ENERAL INFO	
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186	XXXXXX	XXXXX	XXXXXXX	YTXXXXX	II:	WWKTNGPE	SGLSRQE	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	127 XXX	щ.	Дb
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126	- KKQNDVXXXXXXX	; ;		CLNTDI		:       ELRSMMY	XXXXXXX	XXXXXXXXXXXXXXXXQFLRSMMYTFGDYRDICLNTDIS	72 XXX		Db

Search completed: June 20, 2003, 15:07:04 Job time : 18.8255 secs

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RESULT 1 US-10-153-2 Sequence Patent NG GENERAL AF  TT  CC  CC  AP  PF	44444433333333333333333333333333333333
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ication US/101 0169305A1 TION: Sim, Kim L. Sim, Kim L. Chitnis, Chet Miller, Louis Peterson, Dav Su, Xin-Shaun Wellems, Thom NVENTION: BIND SEQUENCES: 37 ENCE ADDRESS: SSEE: Knobbe M T: 620 Newport Beach T. 620 Newport Beach T. 620 Newport Beach T. 620 Newport Beach T. 620 Newport Beach T. 620 Newport Beach T. 620 Newport Newport Beach T. 620 Newport NEWPORT T. GATION DATA CATION NUMBER: GATION NUMBER: GRATION NUMBER: GR	634 634 1118 11338 1338 1497 497 410 380 526 526 527 624 624 627 698 824 428 824 776 776 776
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KAM L.  KAM L.  KAM L.  RIN L.  RIS, Chetan er, Louis. H.  Erson, David S.  Xin-zhaun ems, Thomas E.  ION: BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE  KNODDE Martens Olson & Bear  KNODDE Martens Olson & Bear  KNODDE Martens Olson & Bear  O Newport Center Drive 16th Floor  Ort Beach ifornia  E.  Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS SYSTEM: PC-DOS/MS-DOS PATON DATA:  N NUMBER: US/09/210,288 E: <urknown> ON DATA:  NN NUMBER: US/09/210,288 E: <urknown> ON DATA:  ON NUMBER: 36,516 ON ONDER: NUMBER: NIH121.1FWDV1</urknown></urknown>	US-10-153-668-98 US-10-153-668-100 US-10-153-668-1004 US-10-153-273-14 US-10-153-273-13 US-09-820-843A-107 US-09-820-843A-107 US-09-8134-333-13 US-09-372-348-16 US-10-9815-242-5391 US-09-815-242-5391 US-09-815-242-5391 US-09-726-968-4 US-10-281-478-1 US-09-726-968-4 US-10-281-478-1 US-09-746-968-2 US-09-742-096-3 US-09-742-096-3 US-09-742-096-3 US-10-223-085-336 US-10-223-084-336 US-10-223-084-336 US-10-223-084-336 US-10-223-088-336 US-10-223-098-336 US-10-223-098-336 US-10-223-098-336 US-10-223-098-336
TIUM VIVAX THROCYTE BINDING PROTEINS	Sequence 98, Appl Sequence 100, App Sequence 104, Appli Sequence 14, Appli Sequence 11, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 13, Appl Sequence 13, Appl Sequence 53, Appl Sequence 57, Appl Sequence 57, Appl Sequence 58, Appl Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 36, App Sequence 336, App

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12
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Matches 133; Conservative
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ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION LORDAY.
APPLICATION UMBER: US/09/210,288
FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
FILING DATE: 20nknown>
PRIOR APPLICATION UMBER: US/09/210,288
FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
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FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
FILING DATE: <a href="https://doi.org/10/153/273">https://doi.org/10/153/273</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1646 DPEYKGYEYKDGVQPIQGNEYLLQK 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1528 LTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAERQKK 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 KPEYNSYSKKD-----ASEYLKDK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENIIKDACNEINSTOOC--NDAKHRCNOACRAYOEYVENKKKEFSGOTNNFVLKANVOPO 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDKVEDVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKF--NTEKRQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTNGLSESE-KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKKQ--NDVAKA-KDKIGKFFSKDGSKSPSGLSR-----QEWWKTNGPEIWKGMLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLKDAFIKTAAAETFLSWQYYKSKNDSEAKILDRGLIPSQFLRSMMYTFGDYRDICLNTD 1477
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                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 620 Newport Center Drive CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSCRYIKDTSQTIKSKLG-----DQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.2%;
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Pred. No. 8.1e-48;
""smatches 109;
                                                                                                                                                                                                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bear
16th
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; ORGANISM: Mammalian US-09-924-154-14
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                     Query Match
Best Local Similarity
                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09924154 Patent No. US20020127241A1
           Matches
                                                                                                                                                                                                                                          TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105 CURRENT APPLICATION NUMBER: US/09/924,154 CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/223,525 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                           APPLICANT: Narum, David L. APPLICANT: Sim, Kim L.
                                                                                                                     LENGTH: 1143
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Plasmodium falciparum SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Fuller, michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 QYESQEGKFNTEKR--QKKPEYNSYSKKDASEYLK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682 NYKKOKGRYTEVKKIPLYKEDKDVKNSDDARDYLK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 DIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDD------NKKLQEWWTIHG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
127; Conserv
           85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTEWGENFCKEQKK-EYKV--LLAKCKDCDVDGDGKCNGKCVACKDQCKQYHSWIGIWID 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKV---CKEYENYITGKKT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVIWEGMLCALSYDTSLNNVNPETHKKLTEGNNNFEKVIFGSDSSTTLSKFSERPQFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKIWEGMLCALTNGLS-----ESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DICLGTDISS---KKDTSKGV------GKVKCNIDDVFYKISNSIRYRKSWWETNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-----FINCAAKETHFAWHKYKKD-NVNAEN---ELKSGKIPEGFRKOMYYTFGDFR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
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TELEFAX: (619) 235-0176
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                            2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%;
19.2%; Score 327.5; DB 10; 27.8%; Pred. No. 2.8e-19; tive 46; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Mismatches 106; Indels
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Pred. No. 8.3e-36;
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                                     Length 1143;
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US-10-153-273-6
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Patent No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                          INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                CLASTETYAMTON

COMPATITION DATA:

APPLICATION UMBER: US/10/153,273

FILING DATE: 21-May-2002

CLASTETYAMTON:
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 EYLKDK 308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTSQTIKSKLGDQATTEKGDTHIDDNKKL--QEWWTIHGPKIWEGMLCALTNGLSESEKK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KKDCDENTCKNKCSEYKKWIDLKKSEYEKQVDKYTKDKNKKMYDNIDEVKNKEAN 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKK-PEYNSYSKKDAS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMEENLNKVNKDKKRNE------ESLKIFREKWWDENKENVWKVMSAVLKN------K 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASIYEAQLLKYKYKEKDENALCSI------IQNSYADLADIIKGSDIIKDYYGK 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCNYKSNNEKSWNCTGTFTNKFPGTCEPPRRQTLCLGRTYLLHRGHE----EDYKEHLLG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCNPK-ESYPDWDCKKNIDNSHSGACMPPRRQKLCVRD---LTQGGEIRKPEDILTKFIN
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 620 Newport Center Drive CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Knobbe Martens Olson & Bear ADDRESSEE: Knobbe Martens Olson & The Control of the Floor
                                        STRANDEDNESS: single
                                                               TYPE: amino acid
                                                                                                                                                     TELEFAX: (619)
                                                                                     LENGTH: 749 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92660
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Wellems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peterson, David S.
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                                                                                                                                                     235-0176
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                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Mammalian
US-09-924-154-15
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US-09-924-154-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Narum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
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                                        451 LDVWRDINTNKLSEKFQKIFMGGGNSRKKQ-----NDNNERNKWWEKQRNLIWSSMV--
                                                                                 116 TDI---SSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCA 172
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173 LTNGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLE 232
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                                                                                                                                                                                                                                                          6 NEISGCNPKES--YPDWDC-KKNIDNSHSGACMPPRRQKLC-----VRDLTQGGEIRKP 56
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Pred. No. 2.7e-14;
5; Mismatches 116
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US-10-153-273-21
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                                                                                              Local
                                                                                                                                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/210,288
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION: |
NAME: Fuller, Michael |
REGISTRATION NUMBER: 36,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: NIH121.1FWDV1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                   22 CKKNIDNSHSGACMPPRRQKLC---VRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKY
                                                                              67; Conser
   TYPE: amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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Miller, Louis H.
Peterson, David S.
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BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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RESULT 8
US-09-924-154-13
; Sequence 13, Application US/09924154
; Patent No. US20020127241A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09924154 Patent No. US20020127241A1 GENERAL INFORMATION:
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APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 KKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                 IDKK----VKSPKPSENPSDVATVCNKSCTDYDKWIINKRKEYKMQSSKY---KRDRSLF 398
                                                                                                                                                                                                                        IKAKDYEGCKNNKSNNS----
                                                                                                                                                                                                                                                                                   SEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVC
                                                                                                                                                                                                                                                                                                                       TENILKGNFEGIKANIVSMYPS-YADLSLDEFRK--HWWDQNKKQLWEAISCEFYKG---
                                                                                                                                                                                                                                                                                                                                                     SCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCALTNGLSE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKEKGNDKIWQCINEHIKDFPDVCGPPRRQQLCLGNLDK-DEFKNVND-LKKFLNEIILG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQACRAYQEYVENKK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKVCKEYENYITGKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXXXXXXXXXXXXQFLRSMMYTFGDYRDICLNTDIS-----KKQNDVXXXXXXXX 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXXXXXXXXXKPQFLRWMIEWGEEFCAERQKKENIIKDACXXXXXXXXXXXXK--HRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTEKGDTHIDDNKKLQEWWT1HGPKIWEGMLCAL-TNGLSESEKKNILQDYSYNKLNNA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.48;
24.78;
                                                                                                                                                                                                                                                      ---NHTGVCLMEDDNDNQYLHWFREWKNDFCIDKLKWNDVIKEPC
                                                                                                                                                      308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 262.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                  -CVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 10;
7.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                      345
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                                                                                                                                                                                                                                                                                                                       303
                                                                                                                                                                                                                                                                                                                                                                                                                         119
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; ORGANISM: Mammalian US-09-924-154-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application us Patent No. US20020169305A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105 CURRENT APPLICATION NUMBER: US/09/924,154 CURRENT FILING DATE: 2001-08-07 PRIOR APPLICATION NUMBER: US 60/223,525 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Narum, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
                                                                                                                          ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 NKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 LGDQATTEKGDTHID-DNKKL--QEWWTIHGPKIWEGMLCALTNGLSESEKKNILQDYSY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 KRKYK-----YWNDLS---NKDDKEVCKIINKTFADIRDIIGGTD-----YWNDLS---NRK 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 WECKKPYKLSTKDVCVPPRRQELCL-----GNIDRIYDKNLLMIKEHILAIAIYESRIL 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 WDCKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPED----ILTKFINCAAKETHFA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10153273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --DDNCKRKCNSYKEWISKKKEEYNKQAKQY--QEYQKGNNYKMYSEFKSIKPEVYLK 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPEYNSYSKKDASE---YLK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGKINTNSNYVHRNKQNDKLFRDEWWKVIKKDVW------NVISWVFK------ 610
                                                                                                                                                                                                                                                                                    CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DKTVCKEDDIENIPQFFRWFSEWGDDYCQDKTKM---IETLKVECKE-KPCE-- 658
                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                         STREET: 620 Newport Center Drive
    APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe Martens Olson & Bear
                        APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-08-07
2017
2017
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27.2%;
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Pred. No. 1.6e-13;
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                                                                                                                                 Version #1.25
                                                                                                                                                                                                                                                                                                                                16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Plasmodium vivax SEQUENCE DESCRIPTION: SEQ ID NO: US-10-153-273-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                 US-09-924-154-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-924-154-17
                                                                                                                            SEQ ID NO 17
LENGTH: 1501
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09924154 Patent No. US20020127241A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                    Query Match
Best Local Similarity
                                                                                                                                                                                                              TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105 CURRENT APPLICATION NUMBER: US/09/924,154 CURRENT FILING DATE: 2001-08-07 PRIOR APPLICATION NUMBER: US 60/223,525 PRIOR EILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Narum, David L. APPLICANT: Sim, Kim L.
                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                              NUMBER OF SEQ.ID NOS:
                                                                                                          LENGTH: 1
TYPE: PRT
                                                                                   ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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LENGTH: 1115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GDQATTEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCALTNGLSESEKKNILQDYSYNKLN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 YRYNKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 KKDVCIPDRRYQLCMKELTNLVNNTDTNFHRDITFRKLYLKRKLIYDAAVEGDLLLKLNN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 -VPPCQNACKSYDQWITRKKNQWDVLSNKFISVKNAEKVQTAGIVTPYDILKQELDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 NAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVC---IKAKDYEGCKNNK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 G---TDEKA-----QQRRKQWWNESKAQIWTAMMYSVKKRL----KGNFIWICKLNVAV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 GNSRKNSSNGGNPYDIDHKKTISSAIINHAFLQNTVMKNCNYKRKRRERDWDC-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 HKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 HSGACMPPRRQKLCVRDLT----QGGEIRKPEDIL-----TKFINCAAKETHFAW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fuller, Michael REGISTRATION NUMBER: 36,516 REFERENCE/DOCKET NUMBER: NII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNNSCVKVCKEYENYITGKKTQYESQEGKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (619) 235
(619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
15.2%;
23.4%;
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Pred. No. 1.8e-13
Score 258.5; DB 1
Pred. No. 2.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FCKDIRWSLGDFGDIIMGTDMEGIGYSKVVENNLRSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                    DB 10;
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                      Length 1501
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RESULT 11
US-10-153-273-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10153273 Patent No. US20020169305A1 GENERAL INFORMATION:
                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
                                                                                                                             REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-850
TELEPAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002 CLASSIFICATION: <Unknown>
                 TOPOLOGY:
                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCAAKETHFAWHKYKK--DNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDI---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVDQRR-----KTCER----IDELENMPQFFRWFSQWAHFFCKEKEYWELKLNDK 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Wellems, Thomas E.
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Chitnis, Chetan
Miller, Louis H.
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Su, Xin-zhaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
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US-10-153-273-10
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 INFORMATION FOR
                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
                                                   ATTORNEY/AGENT INFORMATION:
NAME: FULLEY, MICHAel
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sim, Kim L
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ORGANISM: Plasmodium
SEQUENCE DESCRIPTION: SEQ
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79; Conserv
                                                                                                                                                  APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                   TELEFAX:
                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 620 Newport
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STREET: 620 Newport Center Drive 16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Su, Xin-zhaun
Wellems, Thomas E.
INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
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Miller, Louis H
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                   (619)
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             (619) 235-8550
619) 235-0176
NO:
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Pred. No. 1.1e-12;
7; Mismatches 100
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527 74 14;

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ORGANISM: Plasmodium SEQUENCE DESCRIPTION: SEQ US-10-153-273-10
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US-10-153-273-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17,
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Best Local
                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                         APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASS_FICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 NOKKEFLKOKRKYETEISGGGSGKSPKRTKRAARSSSSSDD 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAPYRRLHLCDYNLESIDTTSTTHKLLLEVCMAAKYEGNSINTHYTQH--QRTNEDSA 65
                                                                                                                                                                                                                                                                    STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K---KLENLQKQCRDYEQNLYCSGNGYDCTKTIYKKGKLVIGEHCTNCSVWCRMYETWID 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QATTEKGDTHIDDNK-----KLQE-WWTIHGPKIWEGMLCALTNGLSESEKKNI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
        APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                  OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                Wellems, Thomas E. INVENTION: BINDING D
                                                                                                                                                                                                                                92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peterson, David S. Su, Xin-zhaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                            AND PLASMODIUM: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 237.5; DB 9;
Pred. No. 6.5e-12;
5; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    falciparum
ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                         DOMAINS FROM PLASMODIUM VIVAX SMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                             BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-153-273-15
: Sequence 15, Application U
: Patent No. US20020169305A1
: GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 XCVACKDQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 VCIKAKDYEGCKNNKSNNSCVKVCKEYENYI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 XXXXXXXXXXXXXRPQFLRWLTEWGENFCKEQKK-EYKVLLAKCXXXXXXXXXXXXXX 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 TEKGDTHIDDNKKLQEWWTIHGPKIWEGMLCAL-----TNGLSESEKKNILQDYSYNKL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 ACMPPRRQKLCVRDL--TQGGEIRKPEDILTKFINCAAKETHFAWHKYKKDNVNAENELK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRK-----SWWETNGPVIWEGMLCALXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXXDFKRQMFYTFADYRDICLGTDISS---KKDTSXXXXXXXXXXXXXXXXKISNSIR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTS-----QTIKSKLGDQAT 140
                                                                                                                                           STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fuller, Michael REGISTRATION NUMBER: 36,516
                                                                                                     ZIP: 92660
                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10153273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                        Su, Xin-zhaun
Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221; DB 9;
Pred. No. 6.3e-11;
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Length 324 Indels

66;

Gaps

Version #1.25

16th Floor

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RESULT 15
US-10-139-273-13
; Sequence 13, Application U.
; Patent No. US20020169305A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-153-273-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal
                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
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                                                                                                                                                                                                                                                                                                                                                                                                           205 NSYKEWISKKK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 EKGDTHIDDNKKLQEWWTIHGPKIWEGMLCALTNGLSESEKKNILQDYSYNKLNNAEKDD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 NVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKYKKD 81
                                                ADDRESSEE:
STREET: 620
                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYENYITGKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CXXXXXXIPQFFRWFSEWGDDYCQDKTKMIETLKVECXXX----XC----XDDNCKSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSCVKVC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXNKKNDKLFRDEWWKVIKKDVW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXXXEVCKI-----INKTFADIRDIIGGTD-----YWNDLSNRXXXXXXXXXX 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002
COUNTRY: US
             CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                              Application US/10153273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                           INVENTION: BINDING DOMAINS AND PLASMODIUM F
                                                                                                                                                                              Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
                                                                                                                                                                                                                                                         Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (619)
(619)
                                                EE: Knobbe Martens Olson & Bear 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%;
                                                                                                                                                                Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235-0176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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Pred. No. 1.7e-05;
7; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15:
                                                                                                                           S FROM PLASMODIUM VIVAX
FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- XXXXX 152
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Search completed: June 20, Job time: 33.2489 secs

2003, 15:18:25

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us-10-153-273-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92660
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: NIH121.1FWDV1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: internal
                                      268
                                                                             176 WIREWGRDYVSELPTEVQKLKEKCXXXXXXXXXXXXXVVPPCQN---
                                                                                                                                                               134 WNESKAQIWTAMM
227 ITRKK 231
                                                                                                                    216 WYVEWSDEFCRERKKLEDKVEDVCIKAKDYEG-----CKNNKSNNSCVKVCKEYENY 267
                                                                                                                                                                                                      158 WTIHGPKIWEGMLCALTNGLSESEKKNILQDYSYNKLNNAEKDDCC--LEKFASKPQFLR 215
                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                 98 FRKOMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEW 157
                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                               FCKDIRWSLGDFGDIIMGTDMEGIGYSKXXXXXXXX---XXXTDEKA-----QQRRKQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                      ITGKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                     Score
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Qy 1// LSESE-KRILQD)	5 1236 60 1296 120 1356	RESULT 1 T28075 variant-specific surface protein C;Species: Plasmodium falciparum C;Date: 15-OCt-1999 #sequence_re C;Accession: T28625 R;Su, x.Z.; Heatwole, V.M.; Wert Cell 82, 89-100, 1995 A;Title: The large diverse gene A;Reference number: Z20487; MUJD A;Accession: T28625 A;Status: preliminary; translate A;Molecule type: DNA A;Residues: 1-3006 <sux> A;Cross-references: EMBL:L40609; C;Genetics: A;Gene: var-3 A;Introns: 2597/3 Query Match Best Local Similarity 55.0%; Matches 172; Conservative</sux>	30 108 6.3 433 31 107.5 6.3 219 32 10.7 6.3 1997 33 106.5 6.2 384 35 106.5 6.2 1138 36 105.5 6.2 446 37 105 6.2 1302 38 105 6.2 1302 39 103 6.0 342 40 103 6.0 347 41 103 6.0 807 42 103 6.0 930 43 103 6.0 1025 44 103 6.0 1025 45 103 6.0 11925
E-KKNILQDYSYNKLMNAEKDUCCLEKFASKOOFLEWYVEWSDECKEKKLEDKY	HSGACMPPRRQKLCVRDLTQ  :	3 - malaria parasite (Plasmodium falc vision 15-Oct-1999 #text_change 09-Jun heimer, S.P.; Guinet, F.; Herrfeldt, J family var encodes proteins involved i :95330813; PMID:7606788 d from GB/EMBL/DDBJ NID:9886376; PID:9886377; PIDN:AAA753 NID:9886376; PID:9886377; PIDN:AAA753 Score 894; DB 2; Length 3006; Pred. No. 4.3e-56; Pred. No. 4.3e-56; Pred. No. 4.3e-56; Pred. No. 4.3e-56;	2 T25946 hypotheti 2 T19897 hypotheti 2 F71607 DNA helic 2 F71607 DNA helic 2 F71617 embryonic 2 T18402 asparagi 2 E71615 probable 2 C76608 probable 1 JC6009 surface-1 2 T18474 hypotheti 2 T47561 late embryotheti 2 T47561 late embryotheti 2 T47561 bypotheti 2 T47561 probable anti 2 T47561 probable bypotheti 2 T47561 probable chical surface anti 2 F7451 probable chical surface anti 2 S41649 DNA polym
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RESULT 2
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variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)

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A;Residues: 1-3026 <SMI>
A;Cross-references: EMBL:L42244; NID:g3540144; PID:g3540145; PIDN:AAD03351.1
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A;Title: The large diverse gene family var encodes proteins involved A;Reference number: Z20487; MUID:95330813; PMID:7606788
A;Accession: T28432
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C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T28432
R;Su, X;Z; Heatwole, V.M.; Wertheimer,
                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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                                                                                                                                                                                                                                   Genetics:
                                                                                                                          Matches 122;
                                                                                                                                                                                                                                                                                                                                                                       Smith, J.D.; Kyes, S.; Craig, A.G.; Fagan, T.; Hudson-Taylor, J. Blochem. Parasitol. 97, 133-148, 1998
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                                                                                                                                             Similarity
                                                                                GNDGSNEISGCN-----PKESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRK
                    PEDILTKFINCAAKETHFAWHKYKKDNV
                                               GQDGTKKIEECNTKYYPTKNDYPGWNCTDKVINREEGSCMPPRRQKLCIHNLEHLSEKAT 2055
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                                                                                                                            Conservative
                                                                                                                                       35.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                        Score 600; DB 2;
Pred. No. 6.6e-35;
8; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID: g886374; PID: g886375;
                                                                                                                                                                                                                                                                                                     from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 669.5; DB 2
Pred. No. 6.6e-40;
4; Mismatches 109
                                                                                                                                                                                                                                                                                                                                         from the A4VAR Plasmodium 502; PMID:9879893
                                                                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-Oct-1999 #text_change 09-Jun-2000
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                                                                                                                                                         Length 3026;
                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                         D.;
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                                                                                                                                                                                                                                                                                                                                                    falciparum erythrocyte
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                                                                                                                                                                                                                                                                                                                                                                                         Miller,
                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1525
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T28155
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              variant-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-2706 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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Best Local :
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              surface
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          protein 1 homolog PFB0010w -
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malaria

parasite

(Plasmodium

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variant-specific surface protein 1 - malaria parasite (Plasmodium N;Alternate names: erythrocyte membrane binding protein 1 (EMP1) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Plasmodium falciparum rosetting is mediated A;Reference number: Z20477; MUID:97373957; PMID:92304 A;Accession: T28155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H. Nature 388, 292-295, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2169 NDYGPDIWKGMVCGLSHHIKNGNKEQLRKNLTDNNKYTKISSK-----LEDFASRPQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2056 ETELRKAFIECAAIETFWLWDKYKEDKKDEKKTEGGGISDDPDDPQKKLEGGTIPEDFKR
                                                                                                                                                                         782 NGSIDNCNAKNRKKNEWQCDKNTFVDGNEGVCMPPRKKSICIHNLTLEEQTKNKYQLREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 TIHGPKIWEGMLCALT----NGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQFL
                                                                                                                   DVCIKAKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKP-----
                                                                                                                                                                                                                                                                    --KDVDK-VKKNINKVFNNSSKRGFKKIDP----ENWWNENGPQIWNGMLCALIHADTKD
                                                                                                                                                                                                                                                                                                                                                           FIKCAAKETNLLWDKYKNDKNEAEELLKKGKIPEDFMRIMFYTFGDFRDFCLENDMG----
                                                                                                                                                                                                                                                                                                                                                                                          FINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYESQEGKFNTEKRQKK-----PEYNSYSKKDASEYLKDK
IGIIVKDYVLANAKEYLKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYEQQTAKFDKDKKDKKFDGTSAEVDVAAVSSVHEYLQEE 2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATT--EKGDTHIDDNKKLQEWW 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWYVEWSDEFCRERKKLEDKVEDVCIKAKDYE-GCKNNKSNNSCVKVCKEYENYITGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMFYTYGDYRDFLFGTDISK-----GHGKESALGKKIDSLFKNGDQKSPSGKTPTEWW
                                       -EYNSYSKKDASEYLKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:Y13402;
ce: strain IT
                                                                                    KSIDG-GOLKCDRGCNNKCDEYKKYMRKKKEEWNLQD-KYYKDKRENKGIDKGP
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4/25/5
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Pred. No. 1.3e-29;
9; Mismatches 122;
1085
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A; Residues: 1-1711 <GAR>
A; Cross-references: GB: AE001366;
A; Cross-references: clone 3D7
                                                                                                                                                                                                                                                       A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-2042 <RUB>
                                                                                                                                                                                                                                                                                                                                R;Rubio, J.P.; Thompson, J.K.; Cowman, A.F.
EMBO J. 15, 4069-4077, 1996
A;Title: The var genes of plasmodium falciparum are located A;Reference number; Z18927; MUID:96324414; PMID:8670911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: C71625
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                                                                                                                                                                                                                   C; Genetics
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                                                                                                                                                                                                                                                                                                              A; Accession: T18399
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                                                                                                                    Query Match
Best Local
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                                                                                                  Matches
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                  106; Conser
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                                                        KNIDNSHSG-----ACMPPRRQKLCVRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEDSDVKESKY 1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKERCM-VYQYNGDKGKDDKKEKCTEACTYYKEWLTNWQDNYKKQNQRY-TEVKGTSP-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A---GGKKTLTETYNYSNVTFNGHLTGTKLNEFASRPSFLRWMTEWGDQFCRERITQLQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDC--KKNIDNSHSGA-CMPPRRQKLC-----VRDLTQGGEIRKPEDILTKFINCAAKE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEDVCIKAKDYEGCK-NNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RYIGNDLDKVNNNI--TAVFQNGD-HIPNGQKTDRQRQEFWGTYGKDIWKGMLCALQE 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKL-----QEWWTIHGPKIWEGMLCALTN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYLLWQKYKEDKQNETASTELDIDDPQTQLNGGEIPEDFKRQMFYTFGDYRDLFLG----
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                    RSADGAPSGDKDGAICIPPRRRKLYLHKI-EGVDTTDDKSLRKWF1ESAAVETFFLWDRY
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                                                                                                  Conservative
                                                                                                                23.28;
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                                                                                                  65;
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                                                                                            Score 395; DB 2;
Pred. No. 2.5e-20;
5; Mismatches 109;
                                                                                                                                                                                                                                                                                            from
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Pred. No. 3.8e-23;
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                                                                                                                                Length 2042;
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                                                                                                Indels 124;
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                                                                                                                                                                                                                                                                                                                                                  the subtelomeric region
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N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C;Species: Plasmodium falciparum
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                                      망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Identification of Plasmodium falciparum erythrocyte membrane A; Reference number: Z17860; MUID:98080592; PMID:9419207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chen, Q.; Barragan, A.; Fernandez, V.;
J. Exp. Med. 187, 15-23, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T14029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AF003473; NID: g2961467; PID: g2961468; PIDN: AAC05730.1
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Best Local
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                                      PTYFRWFEEWGESFCRERKKRLKQIKVDCKVENGDVGRCSGDGEACDSISTHDYSTVPSF 1275
                                                                                                                                                                                                                                   KKL----
                                                                                                                                                                                                                                                                     GKIPDGFLRQMFYTLGDYRDILFSGSNDTTSVSKDTPSSSNDNLKNIVLLASGSTE-QER
                                                                                                                                                                                                                                                                                                            GKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDN 151
                                                                                                                                                                                                                                                                                                                                                  PDSKEALLKAFVESAAIETFFLWHRYKEEKKAVAQEGAGHGLPRVEEGSPEYDPEDKLKE 1036
                                                                                                                                                                                                                                                                                                                                                                                        P---EDILTKFINCAAKETHFAWHKYKKD---
                                                                                                                                                                                                                                                                                                                                                                                                                          WRCVTPSGEPTTSSDKNGAICVPPRRRRLYIKKIVDWATKTESPQASGSEASSTSGSTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDC----KKNIDNSHSGA-CMPPRRQKLCVRDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEFDEQKKAYVDRKDKYKTENKGAESKHHSISDQNFVKKLGTDY 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQYESQ-----EGKFNTEKRQKKPEYNSYS----KKDASEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTD-----ISSCRYIKDTSQTIKSKLGD--QATTEKGDTHIDDN--KKLQEWWTI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKLITPQSGSPLLGGWITGVGVENGDDENNPEKLLQKGEIPDGFLRQMFYTLGDYRDILF
                                                                                                                PQKIENPENLWDEANKKPKPPQYQYTNVKLDENSGTSPRTTQTQASSDNTPTTLTHFVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKKRLAQIYEDCRGNDKVCSGDGEDCEEVRKQDYSKISNFNCPGCGRECRKYKNWIKTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKKLEDKVEDVC-----IKAKDYEGCKN----NKSNN----SCVKVCKEYENYITGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGPKIWEGMLCALT ---- NGLSESEKK ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGDKDKKNGYSDIVSGDNVIKERENTIKEKIASFFQNGNKEGTPHVPKNPVQTPQTWWKD
                                                                          PQFLRWYVEWSDEFCRERK-----KLEDKVE--DVCIKAKDYEGCKNNKSNN-----
                                                                                                                                                   -----NGLSESEKKNILQDYSYNKLN-----
                                                                                                                                                                                         EKMNKYKEIKNFRKCSTERSAPNLVSHPQTWWENNGKYIWHGMVCALTSKDKIAKGVEKK
-SCVKVCKEYENYITGKKTQYESQEGKFNTEKRQ-KKPEYNSYSKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 386; DB 2; 1
Pred. No. 1.2e-19;
9; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sundstrom,
                                                                                                                                                                                                                               -QEWWTIHGPKIWEGMLCALT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2228
                                                                                                                                                       ----NAEKDDCCLEKFASK 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138;
                                                                                                                                                                                                                                                                                                                                                                                        - NVNAENELKS
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                                                                                                                                                                                                                               174
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R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P. Cell 82, 89-100, 1958
A:Title: The large diverse gene family var
A;Reference number: Z20487; MUID:95330813,
A:Accession: T28634
                                                                                                  variant-specific surface protein 7 - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 15-Oct_1999 #sequence_revision 15-Oct_1999 #text_change 09 C;Accession: T28634
                  A; Molecule
                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                    В
     A; Residues:
                        A; Status: preliminary; translated
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T28157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: The molecular Reference number: Z20479 Recession: T28157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U31083; NID:g1517813; PID:g1517814; PIDN:AAB06961.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
Tolecule type: DNA
Residues: 1-2212 <YAN>
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  type: DN: 1-2182
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                                                                                                                                                                                                                                                                                              NKKPKDQKYQYDKVKLDENSGTSPKTNDHVPPTPLTNFISRPPYFRYLEEWGETFCRERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                KDEYDKOKEAYNNOKTDARRNNN 1708
                                                                                                                                                                                                                        KTQYESQEGKFNTEKRQKKPEYN
                                                                                                                                                                                                                                            KRLEKIKVECMDEDGKKOKCSGDGEDCEEIRKODYSTVRDFYCPECGKYCRFYKRWIEKK 1685
                                                                                                                                                                                                                                                                      KLEDKVEDVCI-----KAK---DYEGCKNNKSNN-----
                                                                                                                                                                                                                                                                                                                                            VLKNADSQPPSDEKRQTWWEQNGEHTWNGMICALTYKEKDEKGTPLKQNEGLKSALWDEK
                                                                                                                                                                                                                                                                                                                                                                       ----GDTHIDDNKKLQEWWTIHGPKIWEGMLCALT-----
                                                                                                                                                                                                                                                                                                                                                                                                 PPPFLRQMFYTLGDYADIFFGKNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                            SAAIETFFLWDRYKKEKEIEKKEKKVANGGLVPSLNGGPPQQPGVTGDSPQSKLQQTGVI 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAKETHFAWHKYKKDNVNAENELK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNSGSICIPPRRRRLYIQKLHDWASGNTVVSGQAQTPQGGTSSPSGKETPSDKLRTAFIQ
                                                                                                                                                                                                                                                                                                                          EKKNILQDYSYNKLNNAEKDDCC----
                                                                                                                                                                                                                                                                                                                                                                                                                      PEGFRKQMYYTFGDFRDIFFG-TDISSCRYIKDTSQTIKSKLGDQATTEK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHSGA-CMPPRRQKLCVRDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYLK 306
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                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
     <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                        from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 383; DB 2
Pred. No. 2e-19;
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                                                                                  S.P.; Guinet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence
                                                 encodes proteins involved PMID:7606788
                                                                                                                                                                                                                                                                                                                     -----LEKFASKPQFLRWYVEWSDEFCRERK 229
                                                                                                                                                                                                                                                                                                                                                                                               -----VIDTKNGDKDIAEREKKIKDAIER 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TQGGEI-----RKPEDIL-TKFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2212;
                                                                                F.; Herrfeldt,
                                                                                                                                                                                                                                                                     ----SCVKVCKEYENYITGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                       --NGL----SES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128;
                                                                                                           09-Jun-2000
                                                                                                                                 falciparum)
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                                                                                  J.A.; Peterson,
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                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-2647 <HER>
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                                                                                                                                                        A; Note:
                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                           R; Hernandez-Rivas, Mol. Cell. Biol. 1
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                                                                                                                   Similarity
SAAIETFFLWDRYKKGKAIAKKEKKKQMVDYSPLSTADPHNNPVSLVIAPNPNYNKTCVI
                             CAAKETHFAWHKYKKDNVNAENELKSGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT----NGLS-
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                                                                                                       Conservative
                                                                                                                                                                                                                                                                                       17, 604-611, 1997
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                                                                                                                21.2%; 27.4%;
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A;Title: Expressed var genes are found in Plasmodium falciparum A;Reference number: Z20483; MUID:97154495; PMID:9001213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein FCR3-varT11-1 - malaria parasite (Plasmodiu C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:L42636; NID:g886379; PID:g886380; PIDN:AAA75399.1 C;Genetics: A;Note: var-7
SNSGSICIPPRRRRLYIQKLHDWASGNTVVSGQAQTPQGGTSSPSGKETPSDKLRTAFIQ
                                              SHSGA-CMPPRRQKLCVRDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASGSTEQEKEKMKQIQAKIKKILNGATSGVPPVTKNSVKTPQQTWWENIAKDIWNAMVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNVLQDLSSSCAKPCRLYKTWIEKKKTEYEKQQKAYEQQKSNYENEQKDKCQTQSNNNAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPQTQLQQTGVIPPDFLRQMFYTLADYKDILYSGSNDTSDTTGKQTPSSSNDNLKNIVLE
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                                                                                                                                                                                                                                    EMBL:U67959; NID:g1794255; PID:g1809295; PIDN:AAC47438.1 ce: strain FCQ27/PNG
                                                                                 Score 361.5; DB 2;
Pred. No. 8.7e-18;
""smatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sterkers, Y.; Peterson,
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                                            -TQGGEI-----RKPEDIL-TKFIN
                                                                                        Indels 135;
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variant-specific surface protein - malaria parasite (Plasmodium falciparum) (fragments) (;Species: Plasmodium falciparum C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000 C;Accession: T14602 R;Voss, T.S.; Felger, I.; Weiss, N.; Beck, H.P.
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A; Residues: 1-2135 < VOS>
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A; Accession: T14602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Voss, T.S.; Felger, I.; Weiss, N.; Beck, H.P. submitted to the EMBL Data Library, February 19
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                                                                                                                                                                                                                                                                                                                                           TIKSKLGDQATTEKGD-----THIDDNKKL-QEWWTIHGPKIWEGMLCALTNGLSESEK 182
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                       KKDASEYLK
                                                            IDCRDCYKECRKYKKWVHKKFDEFHNQKNKYG-EEHEKLTNGDNYSGGGDNTNFCQQIKE
                                                                                                                                                YFRYLEEWGQNFCKTRKRM--
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                                                                                                  ----SCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPEYNSYS---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ILTKFINCAAKETHFAWHKYKKDNV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 354; DB 2; Pred. No. 2.4e-17;
                                                                                                                                                                                                                                                                  -DYS-YNKLNNAEKDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g2944094; PID:g2944095; PIDN:AAC05220.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KSGEPTGGSICIPPRRRKLYVGGLTKWAEIQSSQSQAL 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VIDTKNGDKDIAEREKKIKDAIER 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SKPQFLRWYVEWSD
                                                                                                                                                                                                                                                                  ---CCLEKFASKPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                             -RYIKDTSQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium
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                                                                                                    297
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          A; FICLE: Chromosome 2 sequence of the human malaria parasite A; Reference number: A71600; MUID:99021743; PMID:9804551 A; Accession: B71600
                                                                           R;Gardner, M.J.; Tettelin, H.
; Pertea, M.; Salzberg, S.;
Science 282, 1126-1132, 1998
                                                                                                                                                                                variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium N;Alternate names: erythrocyte membrane binding protein 1 (EMP1) C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
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A;Title: The large diverse gene family var A;Reference number: Z20487; MUID:95330813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant-specific surface protein 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                               в71600
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A; Introns: 2197/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-2664 <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T28626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T28626
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                          C; Accession: B71600
                                                                                                                                                           C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GNDG-----SNEISGCNPKESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKTAEDFLK 1832
                                                                                                                                                                                                                                                                                                                          QANAYSKQKTKYEEGSKGAGLNDHNKEFCVKLGTCTDAAAFL 1770
                                                                                                                                                                                                                                                                                                                                                                  QEGKENTEKRQ----KKPEYNSYSKK---
                                                                                                                                                                                                                                                                                                                                                                                                        KQIKEECMDGSDKKYSGDGEQCDRRDTSNEVSADLEGRSCGNSCRFYKKWIKRKRKEYDK 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                              DKVEDVCIKAKD--YEG----CKNNKSNN-----SCVKVCKEYENYITGKKTQYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTYKTQYDYEKVKLEDTSGAKTPSASSDTPLLSDFVLRPPYFRYLEEWGQNFCKERKKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWTIHGPKIWEGMLCALT------NGLSESE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGNTSDSGNTNGSNNNNIVLEASGNKEDMQKIQEKI-EQILPKNGGTPLVPKSSAQTPDK 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKEWLAQKKAELQNGGLDLYSSGDGDPDNPQNKLLNGVIPPDFLRLMFYTLGDYRDILVH 1489
                                                                                                Tettelin, H.; Carucci, alzberg, S.; Zhou, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KKNILQDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.6%; pred. No. ...
23.6%; pred. No. ...
"Type 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 352; DB 2;
Pred. No. 4.3e-17;
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                                                                                                    Sutton,
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                                                                                                  D.J.; Cummings, L.M.; Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.P.; Guinet, F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123;
                                                                                                                                                                                                                                                                                                                                                                  -DASEYL 305
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                                                            Plasmodium falciparum
                                                                                                  Aravind, E
R.; White,
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                                                                                                  Koonin, l
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-HIDDNKKLQEWW

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                                                                                                                                                                                                                    A; Cross-references: EMBL:U27338;
                                                                                                                                                                                                                                                                                  A;Reference number: Z18925; MUID:95330812; PMID:7541722
                                                                                                                                                                                                                                                                                                                  R;Baruch, D.I.; Pasloske, B.L.; Singh, Cell 82, 77-87, 1995
A;Title: Cloning the P. falciparum gene
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-2924 <
                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                variant-specific surface protein 1 - malaria parasite (Plasmodium N;Alternate names: erythrocyte membrane binding protein 1 (EMP1) pecies: Plasmodium falciparum pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09
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A;Residues: 1-2197 <GR>
A;Cross-references: GB:AE001434;
A;Experimental source: clone 3D7
C;Genetics:
                                                                                                                                                                                        Gene: EMP1
                                                                                                        Matches 105;
                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                      Similarity
                               KTAPTSWKCIPSGNNTTTESTTKPGAAGTPSGKDTGSICVPPRRKLIYVGKLHDWAGGET 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
        ----TQGGE--
                                                                   KESYPDWDCKKNIDNSHS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDESGEKRPDSSASGTKLTDF1KRPPYFRYLEEWGENFCKKRTEMLGK1KEDCYKNGGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDYSYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRIAEHVWHGMVCALTYKDDDNGLKGVVKKPQKIENPEKLWNETTKKPKDEKYQYQTAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDKNGGNNIILNASGNKDEKQKMEKIQEKI-EQILPTSGNKETRGPQNSVNDRQSL---W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPGGKERFPNWKCVSSGEKSVATAGSSGATGKSGDKGAICVPPRRRRLYVGGLTKLTSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIHGPKIWEGMLCALT ----NGL ------
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                         <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GTDI----SSCRYIKDTSQTIKSKLGDQATTEKGD-----THIDDNKKLQEWW 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - AKDYEGCKNNKSNNSCVKVCKEYENYITGKKTQYESQEGKFNTEKRQKKP
                                                                                                                 . 18.2%;
23.0%;
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                                                                                                    ;09
                                                                                                                                                                                                               NID:g914918; PID:g914919; PIDN:AAB60251.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                             Score 311; DB 2;
Pred. No. 4.3e-14;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE001362; NID:g3845341; PIDN:AAC71996.1; PID:g38453
                                                                                                                                                                                                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 342.5; DB 2;
Pred. No. 1.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DNVNAENEL-KSGKIPEGFRKQMYYTFGDFRDIFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1729 <B
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                                                                                                   DIVGDTIVSITEGESTKKKISKIIEGFLKKQTVTSPSPRDTSSRTPVHPQTSVEKTPQ-Q
                                                                                                                                                                     QHGAGATGLQLPGVTVDDSDPDPQTQLKRGNIPNDFLRQMFYTLGDYRDICIGGD----R
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Pred. No. 1.9e-13;
5; Mismatches 126;
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 -LEKFASKPQFLRWYVEWSDEFCRER-KKLEDKVEDVCI 240
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complet me : 26.	1275	275	1215	241	1155
Search completed: June 20, 2003, 15:06:23  Job time : 26.3035 secs	1275 FTEQEKAFPKOKDYYVNGNNKGGGDNGFCITLKSLSDAAQFLE 1317		1215 GENGYGRGRKOKTPOCSCYGEDCEDOLSKYSYDTVADLECPKCAKHCRWYKKWIEKKKDE 1274		1155 SSAMPTSSSSSSGSNDPINTPKLTEFVEIPTFFRYLHEWGQNFCKERMKRLKQIYKECKV 1214

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OM protein - protein search, using sw model

Run on: June 20, 2003, 14:37:29; Search time 13.5539 Seconds (without alignments)

942.514 Million cell updates/sec

Title: Perfect score: US-10-087-013-11 1706 1 GNDGSNEISGCNPKESYPDW......KKPEYNSYSKKDASEYLKDK 308

Scoring table: BLOSUM62

Searched:

Gapop 10.0 , Gapext 0.5

al number of hits satisfying chosen parameters:

112892

112892 segs, 41476328 residues

Minimum DB Maximum DB seg length: 0 seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1070 1070 1003 1025 1070 134 179 676 676 743 785 936

EXTRACELLULAR (POTENTIAL).
POTENTIAL. DUFFY RECEPTOR, GAMMA FORM.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

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208 NNVMDKCNDKRKRGERDWDCPTEKD-----VCIPDRRYQLCMMEIT----

5 SNEISGCNP--KESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDILTK 62

63 FINCAAKETHFAWHK---YKKD-----NVNAENELKSGK----IPEGFRKQMYYTFG 107

Query Match 15.9 Best Local Similarity 27.5 Matches 90; Conservative

15.9%; 27.5%; 120931 MW;

39;

Score 271.5; DB 1; Pred. No. 4.2e-12; 9; Mismatches 117;

Indels Length 1070;

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# ALIGNMENTS

RESULT 1 PVDG_PLA ID . PVD AC P50 DT 01- DT 01- DT 01- DT D1- D1- DT D1- DT D1- DT D1- DT D1- DT D1- DT D1- DT D1- DT D1- DT D1-	RESULT 1  ID PVDG_PLAKN STANDA  AC P50494;  DT 01-OCT-1996 (Rel. 34,	STANDARD;  (Rel. 34, Cz (Rel. 34, La (Rel. 34, La cor, gamma fc cor, gamma fc cor, gamma fc	· AR	D; PRT; 1070 AA.  Created)  Cast sequence update)  Last annotation update)  form precursor (Erythrocyte binding protein).	1070 AA. update) n update; (Erythr	· · · · · · · · · · · · · · · · · · ·	bindin
R R R O	NCBI_TaxID=5850; [1] [SEQUENCE FROM N.A. MEDLINE=92357776; Pub	950; M N.A. 7776; Pu	1, APICO	red=1496004;	raciiiCoppo		Fasinoa
RA RT	Adams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller L.H.; "A family of erythrocyte binding proteins of malaria parasites.";	Sim B.K. erythro	cyte bi	S.A., Fa	ng X., oteins o	Kaslow f malar	D.C., ia par
3 8	-:- FUNCTION: BINDS TO THE HUMAN ERYTHROCYTES DUFFY BLOOD GROUP	ACAC. SO	TO THE	A. 89:/08	THROCYT	1992). ES DUFF	Y BLOO
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3 6		LAR LOCA	TION: T	SUBCELLULAR LOCATION: Type I membrane protein.	nbrane p	rotein.	
88	SIMILAKI	LI: HIGH	1, 10 F.	SIMILARITY: HIGH, TO F.VIVAX DUFFY RECEPTOR.	THE KECE	TIOX.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	ROT enti	cy is co	pyright.	It is p	roduced	throu
8	between the Swiss Institute of Bioinformatics and the EMBL outstation -	Swiss ]	Institut	e of Bioi	informat	ics an	d the
88	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	Bioinfo -profit	ormatics instit	<pre>pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way</pre>	e. The	re are as its	no re conten
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38	or send an email to license@i	mail to	license	@isb-sib.ch).	.ch).		 
DR	EMBL; M90695; AAA29604.1; -	: AAA296	504.1; -	•			
ΚW	Malaria; Receptor; Glycoprotein; Signal; Transmembrane;	eptor; (	lycopro	tein; Sig	nal; Tr	ansmemb	rane;
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NCBI_TaxID=126793;
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Eukaryota; Alveolata; Apicomplexa; Ha
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Erythrocyte-binding antigen EBA-175.
Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBI_TaxID=5835;
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gen 175 in Plasmodium falciparum.",
Biochem. Parasitol. 41:293-296(1990).
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Pred. No. 1.7e-J
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-i- FUNCTION: BINDS TO THE HUMAN ERYTHROCYTES DUFFY BLOOD GROUP
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            NEISGCN--PKESYPDWDC--KKNIDNSHSGACMPPRRQKLCVRDLT--
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Pred.
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CYTOPLASMIC (POTENTIAL)
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PVDA_PLAKN
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P22545;
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                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=92357776; PubMed=1496004; Adams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller "A family of erythrocyte binding proteins of malaria parasites. Proc. Natl. Acad. Sci. U.S.A. 89:7085-7089(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium knowlesi.
Fukaryota; Alveolata;
                                                                                        EMBL; M90466; AAA29602.1;
EMBL; M68517; AAA29590.1;
EMBL; M68518; AAA29591.1;
PIR; A35970; A35970.
                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                use
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the micronemes of invasive
                                                                                                                                                                                                                                                                                                               Aikawa M., Miller L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: HIGH, TO P.VIVAX DUFFY RECEPTOR.
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.H., Hudson D.E., Torii M.,
                                                                                                                                                          requires a license agreement
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DUFFY RECEPTOR, ALPHA FORM.
EXTRACELULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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   use by modified
                                                                                                         MEDLINE=96051398; PubMed=7584044; Sexuka T., Tanaka A., Sexuka N., Nagase T., Miyajina N., Sazuka T., Tabata S.; Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0041-KIAA0080) canalysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.1.
thiolesterase 8) (Ubiquitin-specific processing
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MEDLINE=96051398; P
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                    between
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                                                                                                                                                                                                                                                        (Deubiquitinating enzyme 8). USP8 OR KIAA0055.
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                                                                            Res. 1:223-229(1994).
CATALYTIC ACTIVITY: Ubiquitin
ubiquitin + a thiol.
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                                                                   SIMILARITY: BELONGS
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                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
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    not
          ght. It is produced through a collab
Bioinformatics and the EMBL outsit
Bioinformatics and the restrictions
titute. There are no restrictions
ns as long as its content is in
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No. 6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CVKVCKEYENYITGKKTQYESQEGKFNTEKRQ
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                                                                                                                                                                                                                       Hominidae;
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Best Local S
Matches 66
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                                                                                                                                                             ATRX_HUMAN STANDARD; PRT; 2492 AA. P46100; P51068; Q1886; Q9NTS3; Q9H0Z1; O1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last seguence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
              "ATRX
                           Gibbons R.J.;
                                   Picketts D.J.,
                                             VARIANTS ATR-X. MEDLINE=97123494; Pubmed=8968741;
                                                                                                                                          nuclear protein) (XNP) (Znf-HX). ATRX OR RAD54L OR XH2.
                                                                      SEQUENCE FROM N.A.
                                                                                                                                Homo sapiens (Human)
                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ubl conjugation pathway: Hydrolase; Thiol ACT_SITE 1059 . BY SIMILARITY ACT_SITE 1059 . BY SIMILARITY ACT_SITE 1067 1067 BY SIMILARITY
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PROSITE; PS00972; UCH_2_1;
PROSITE; PS00973; UCH_2_2;
PROSITE; PS00973; UCH_2_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00442; UCH-1; 1. Pfam; PF00443; UCH-2; 1. Pfam; PF00581; Rhodanese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; C19.011; -.
Genew; HGNC:12631; USP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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              encodes a novel
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56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA06225.1; -.
                                   Higgs
                                                                                                                                                                                                                                                                                                                                                                                                        -CLEKFASKPQFL---RWYVEWSDEFCRERKKLEDKVED---
  mechanism
                                                                     (ISOFORMS 1;
                                                                                                         Chordata;
Primates;
                                   D.R.,
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21.6%;
member of the SNF2 hanism underlying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127523 MW;
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                                   Bachoo S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                         Craniata; Ve Catarrhini;
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                                  Blake D.J.,
  the ATR-X
                                                                     AND
                                                                                                                   Vertebrata;
             family of
                                                                                                         Hominidae;
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                                                                     5),
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                                                                      VARIANT
of proteins: syndrome.";
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                                  Quarrell O.
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                                                                                                                    Euteleostomi;
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                                                                     S-1860,
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           mutations
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"Cloning X-linked
                                                                                                                                                                                                                                   MEDLINE-20040663; PubMed-10570185;
McDowell T.L., Gibbons R.J., Sutherland H., O'R.
Bickmore W.A., Pombo A., Turley H., Gatter K.,
Buckle V.J., Chapman L., Rhodes D., Higgs D.R.;
"Localization of a putative transcriptional reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibbons R.J., Picketts D.J., Villard L., Higgs D.R.; "Mutations in a putative global transcriptional regulator cause X-linked mental retardation with alpha-thalassemia (ATR-X syndrome).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gecz J., Pollard H., Consalez G., Villard L. Millasseau P., Khrestchatisky M., Fontes M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stayton C.L., Dabovic B., Gulisano M., G
Giovanazzi S., Bossolasco M., Monaco L.,
                                                                                                                           Villard L., Fontes M., Ades L.C., Gecz J.;
"Identification of a mutation in the XNP/AT
reported as Smith-Fineman-Myers syndrome.";
                                                                                                                                                               MEDLINE=20213147; PubMed=10751095;
                                                                                                                                                                             DISEASE
                                                                                                                                                                                                            pericentromeric heterochromatin
chromosomes.";
                                                                                                                                                                                                                                                                                               HETEROCHROMATIN.
                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                               Hum. Mol.
                                                                                                                                                                                                                                                                                                                                                                   Colleaux L.;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98167853; PubMed-9499421; Cardoso C., Timsit S., Villard L.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pearce
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1375-2492 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 80:837-845(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2401-2492 FROM N.A., AND VARIANTS MEDLINE=95211835; PubMed=7697714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94214473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of a putative helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bianchi M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95179111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Determination of the genomic structure of the a potential zinc finger helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colleaux L., Schwartz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97386582; PubMed=9244431;
Villard L., Lossi A.-M., Cardoso C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                              without
                                                                              MEDLINE=97196774;
                                                                                            VARIANT ATR-X
                                                                                                                                                     Villard
                                                                                                                                                                                                                                                                                                                                                     "Specific interaction between the XNP/ATR-X
             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol.
                                                                                                                                                                                                                                                                                                                                            of the human
                                                                    Ľ.,
                                             alpha-thalassemia.";
            JM GLN-2131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and expression of the murine homologue of a nuclear protein gene closely linked to PGK1 . Genet. 3:39-44(1994).
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                                                                    Lacombe D.,
                                                                                                                                                                                                    Acad.
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                                   Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 FROM N.A.
Pubmed=7874112;
                                                                    PubMed=9043863;
be D., Fontes M.;
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PubMed=8630485
                                                                                                                  91:83-85(2000).
                                                                                                                                                                                                                                                                                                                                            EZH2
                                  4:316-320(1996)
                                                                                                                                                                                                                                                                                                          AND
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                                                                                                                                                                                                 96:13983-13988(1999)
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+s D.J.,
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                                                       ATR-X
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Wada T., Kubota T., Fukushima Y., Saitoh S.;

Wolecular genetic study of japanese patients with X-
alpha-thalassemia/mental retardation syndrome (ATR-X)
Am. J. Med. Genet. 94:242-248(2000).

-i- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGUL
GENE EXPRESSION BY AFFECTING CHROMATIN. MAY BE IN
BRAIN DEVELOPMENT AND FACIAL MORPHOGENESIS.

-i- SUBBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN
                                                                                                                                                                                                                                                                                                                                                                              Villard L., Bonino M.-C., Abidi F., Ragusa A., Belougne J., Villard L., Bonino M.-C., Bonnefont J.-P., Romano C., Fichera | Lossi A.-M., Seaver L., Bonnefont J.-P., Romano C., Fichera | Lacombe D., Hanauer A., Philip N., Schwartz C.E., Fontes M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Villard
Munnich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mutation of the XNP/ATR-X gene in a family with severe mental retardation, spastic paraplegia and skewed pattern of X inactivation: demonstration that the mutation is involved in the inactivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genotype/phenotype relationship in Hum. Mutat. 12:214-214(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20123062; PubMed=10660327;
Fichera M., Romano C., Castiglia L., Failla P., Ruberto C
Greco D., Cardoso C., Fontes M., Ragusa A.;
"New mutations in XNP/ATR-X gene: a further contribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutations in transcriptional resignificance of a PHD-like domai Nat. Genet. 17:146-148(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97467722; PubMed-9326931;
Gibbons R.J., Bachoo S., Picketts D.J., F
Bergoffen J., Berry S.A., Dahl N., Fryer
Levin M.L., Masuno M., Neri G., Pierpont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "XNP
                                                                                                                                                                                                                                                                                                   VARIANTS ATR-X S-179; L-190; I-194
MEDLINE-20451413; PubMed=10995512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abidi F., Schwartz C.E., Carpenter Curtis M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99219535; PubMed=10204841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99326061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99347960;
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                                                                                                                                                                                                                                                                                                                                                             'Evaluation of a mutation screening strategy for sporadic arm-x syndrome.":
                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS ATR-X E-175; 178-V--K-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Carpenter-Waziri syndrome results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lossi A.-M., Millan
        ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF X-LINKED ALPHI
THALASSEMIA/MENTAL RETARDATION SYNDROME (ALSO KNOWN AS I
SYNDROME). ATR-X IS AN X-LINKED DISORDER COMPRISING SEVI
PSYCHOMOTOR RETARDATION, FACIAL DYSMORPHISM, UROGENITAL
ABNORMALITIES, AND ALPHA-THALASSEMIA. AN ESSENTIAL PHENCE
                                                                                                          INTERACTING WITH HP1.
ALTERNATIVE PRODUCTS:
                                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                                                similarity).
                                                                                                                                     HETEROCHROMATIN DURING
                                                                                                                                                                             PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT
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 HEMOGLOBIN H
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an J.M., Villard L.,
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                                                                                                                                     AND MITOSIS,
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 INCLUSIONS
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Keppler K., Kurosawa
., Slaney S.F.,
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                                                                                                                                                                                                                                   REGULATOR. MODIFIES
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              PHENOTYPIC
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U72937; AAB49970.2; -. EMBL; U72938; AAB49971.2; -. EMBL; U72935; AAB40698.1; -. EMBL; U72904; AAB40698.1; JO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN ATRX ARE A CAUSE OF SMITH-FINEMAN-MYERS SYNDROME (SFM). CLINICAL FEATURES INCLUDE SEVERE MENTAL SYNDROME (SFM). CLINICAL FEATURES INCLUDE, FACIAL ANOMALIES AND BILATERAL CRYPTORCHIDISM, DUE TO THE CLINICAL OVERLAP MITH ATR-X SYNDROME, SOME PATIENTS ORIGINALLY DIAGNOSED AS HAVING SFM, MIGHT BE AFFECTED BY A VARIANT OF ATR-X SYNDROME WHICH LACK HEMOGLOBIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF CARPENTER-WIZIRI SYNDROME (CWS), AN X-LINKED RECESSIVE CONDITION CHARACTERIZED BY MODERATE MENTAL RETARDATION, SHORT STATUTURE, BRACHDACTYLY WITH EXCESSIVE SKIN CREASES, AND WIDENING OF THE KNUCKLES.
DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF JUBERG-MARSIDI SYNDROME (JM). JM IS A RARE X-LINKED RECESSIVE DISEASE CHARACTERIZED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATURE AND CRYPTORCHIDISM.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF SUTHERLAND-HAAN X-LINKED MENTAL RETARDATION SYNDROME (SHS). IT IS CHARACTERIZED BY SEVERE MENTAL RETARDATION WITH SPASTIC PARAPLEGIA, MICROCEPHALY, SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEVERE MENTAL RETARDATION, GROWTH FAILURE, SENSORINEURAL MICROGENITALISM AND EARLY DEATH.
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AAB40698.1; JOINED.
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Moliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Mylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,
RA Mylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.V., Carizado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G. V., Ussery D., Barrell B.G., Nurse P.;
RT Nature 415:871-880 (2002)
RESTORD RESTORTS HILL RESTORTS HILL
C. --- STRILBATTY- SOME. TO HISTON
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C13G7.03 in chromosome I
SPACI3G7.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
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Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=972;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical content is supported to the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005120;
Pfam; Pf03467; Smg4_U
Hypothetical protein
SEQUENCE 278 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                          165 IWEGMLCALTNGLSESEKKNILQDYSYNKLNN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                        TFGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPK
                                                                                                                                                                                                                                                 PEQVFLQSINSFL--PHVEWHRFSKGKATVGTRSELLSFAYLKFQSATAVQEFFRVYQGH
                                                                                                                                                                                                                                                                                                                     PEDILTKFINCAAKETHFAWHKYKKD--NVNAENELKS------GKIPEGFRKQMYY
                                                                                                       TFIDKKNNTYRAIVTIAPYQKIPPSKVKA-----
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smg-4_UPF3.
                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100;
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                                                                                                           -DSLEGSLEQDPKFQEF-----K
-AEKDDCCLEKFASKPQFLRW
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                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q92120;
Q92120;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosi
                                                                                                                                                      MGD; MGI:1929095; Vdp.
InterPro; IPR000225; Armadillo.
InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of mouse TAP (transcytosis associated protein/pl15).";
Submitted (OCT-1998) to the EMBL/GenBank/DDA databases.

1- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR
INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR
TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO
THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY
INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
AND TARGET MEMBRANES IN PROXIMITY (BY SIMILARITY).

1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES
BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             EMBL; AF096868; AAC72967.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Han S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                     SEQUENCE
                                                                                                 NON_TER
                                                                                                            Phosphorylation.
                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDP_MOUSE
                                                             DOMAIN
                                                                                     DOMAIN
                                                                                                                       ransport;
                                                                                                                                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TA COIL, AND A HIGHLY ACIDIC C-TERMINAL DOMAIN. ETM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;
                                                                                                                                                                                                                                                                                                                   SIMILARITY; BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS. DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE, PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
DOMAIN: COMPOSED OF A GLOBULAR HEAD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                              SM00325; RhoGEF;
                                                                                                                      PS50176; ARM_REPEAT;
t; Protein transport;
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                              941 AA;
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19.6%;
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  Score
Pred.
                                                           GLOBULAR HEAD.
COILED COIL (POTENTIA
ASP/GLU-RICH (ACIDIC)
                                    PHOSPHORYLATION (BY AB5C10895CD7E508
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                                                                                                                      UNKNOWN_1.
Golgi stac
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 99.5; DI
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                                                                                                                      stack;
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                                                                                                                                                                                                                                                     There are no restrictions ong as its content is in
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                                                                      (POTENTIAL).
            DB
                                                                                                                      Membrane;
                                                                                                                                                                                                                                          Usage
            1;
                                    SIMILARITY).
CRC64;
            Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
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; Murinae; Mus
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Query Match
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RESULT 10
YY02_METJA
ID YY02_METJA
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q60301;
01-NOV-1997
                                                                 Hypothetical protein; Transmembrane; TRANSMEM 837 857 POTENTI
                                                                                                     InterPro; IPR002296; N12N6_mtfrase.
InterPro; IPR002052; N6_Mtase.
PRINTS; PR00507; N12N6WTFRASE.
PROSTTE; PS00092; N6_MTASE; 1.
                                                                                                                                                                                                     EMBL; L77119; AAC37060.1; TIGR; MJECS02; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JAL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome
                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: WEAK IN METHYLTRANSFERASES.
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P32380;
01-OCT-1993
                                                                                                                                                                        Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Paulley A., Peluso D., Rifken L., Riles L., Talch A., Trevaskis E., Vignati D., Rifken L., Rohldman P., Vaudin M., Wilson R., Waterston R.; Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.; Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEOSKELETON. POTENTIAL ROLE IN CROSSLINKING FILAMENTS OR ANCHORING OTHER MOLECULES. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A spacer protein in the Saccharomyces cerevisiae whose transcript is cell cycle-regulated.";
J. Cell Biol. 123:1175-1184(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The NUF1 gene encodes an essential coiled-coil related is a potential component of the yeast nucleoskeleton.", J. Cell Biol. 116:1319-1332(1992).
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16-CCT-2001 (Rel. 40, Last annotation update)
NUF1 protein (Spindle poly body spacer protein
NUF1 OR SPC110 OR YDR356W OR D9476.3.
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                       This
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                                                                                                         IS ESSENTIAL FOR GROWTH SUBCELLULAR LOCATION: NI NUCLEUS. IT IS PRESENT:
                                                               PTM: MAY BE REGULATED BY PHOSPHORYLATION EVENTS
SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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cetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                           EXCLUDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poly body
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  collaboration
outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
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ID SMC2_
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STRAIN-S288c
                                                                                         family
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Query Match
Best Local S
Matches 81
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EMBL; X73297; CAA51733.1; -.

EMBL; U28372; AAB64791.1; -.

PIR; S26710; S26710.

PIR; S24288; S34288.

SGD; S0002764; NUF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        SMC2_YEAST P38989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, 01-FEB-1995 (Rel. 31, 15-JUN-2002 (Rel. 41,
                                                                Strunnikov A.V., Hogan E., Ko
"SMC2, a Saccharomyces cerevi
segregation and condensation,
                                                                                                                                                                                                                                                 Chromosome segregation SMC2 OR YFR031C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil;
               Genes Dev. 9:587-599(1995)
                                                                                                                                                                                            Eukaryota; Fungi; , Saccharomycetales;
                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                       MEDLINE=95212908; PubMed=7698648;
SEQUENCE FROM N.A
                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKYSKM-----EKELKEREFNYKISESKLEDEKTTLNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQYESQEGKFNTEKRQKKPEYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WYVEWSDEFCRE-RKKLEDKVEDVCIKAKDYEGCKNNKSN--NSCVKVCKEYENYITGKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSQLIAKEGKLASLMAQLTQLESKLNQRD----SQLGSREEE----LKKTNDKLQKDIRIAR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPKI--WEGMLCALTNGLSESEKKNILQDYSYNKLNNAEKDDCCLEKFASKPQ----FLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDEMDLQLKQKQNESKRLKDELNELETKFSENGSQSSAKENELKMLKNKIAELEEEISTK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFRDIFFGTDISSCRYIKDTSQTIKSKL---GDQATTEKGDTHIDDNK--KLQEWWTIH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEDILTKFI - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEDELKNLMNELNELKSNAEEKDTQL - - - EFKKNELRKRTNELNELKIK -
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944 7
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                                                                                                                                         N.A.
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                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                             Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
731
747
                                                                                                                                                                                            Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomycetaceae;
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                                                      n E., Kosman, serevisiae gene f
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
n protein SMC2 (DA-box p
                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NCAAKETHFAWHKYKKDNVNAE-NELKSGKIPEGFRKQMYYTF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97.5;
Pred. No. 1
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1; 04FAA074BB8A0BC8
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                                                                    essential for characteristics a subgroup within
                                                                                                                                                                                                Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    SMC2)
                                                                     chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TQGGEIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                       Prodom; PDOUUUUU,
Prodom; PDOUUUUU,
Mitosis; ATP-binding; Coi
NP_BIND 32 39
NP_BIND 172 469
NOMAIN 678 1027
                                                                                                                                                                                                                                                   dery Match
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eki T., Naitou M., Hagiwara H., Abe M., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Shibata T., Wtanabe K., Ono A., Yamazaki M.-A., Tashiro H., Hanaoka T., Murakami Y.; "Fifteen open reading frames in a 30.8 kb region of the right arm chromosome VI from Saccharomyces cerevisiae."; Yeast 12:177-190(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINU:
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami Y., Nai
Sasanuma S.-I.,
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96287654; PubMed=8686381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD PART OF A CHROMOSOME CONDENSATION MOTOR. SUBUNIT: HOWODIMER OR HETERODIMER WITH SMC1 OR OLIGOMERS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                             $48530; $48530.
$0001927; $MC2.
                              241
                                                                         186
                                                                                             344
                                                                                                                    134
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                                                     394
                                                                                                                                       288 KEKELHKEGTISKLENKEN----GLLNEISRLKTSLSIKVENLNDTTEKSKALESEIASS
                                                                                                                                                                                                                                                                                                                                                                                                                U05820; AAA17416.1; -. D50617; BAA09270.1; -.
                                                                                                                                                                                                        25
                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                        Similarity
                              KAKDYEGCKNNKSNNSCYKVCKEYENYITGKKTQYESQEGKF-NTEKRQKKPEYNSYSKK
                                                                                                                                                             AENEL-KSGKIPEGFRKQMYYTFGDFRDIF-FGTDIS-SCRYIKDTSQTIKS
                                                                                                                                                                                  NIKHKHTS-----IRETLENGETRM--KMLNEFVKKTSEEIDSLNEDVEEIKLQ
                                                                                                                                                                                                      NIDNSHSGACMPPRRQKLCVRDLTQGGEIRKPEDILTKFINCAAKETHFAWHKYKKDNVN
          EPKLKEATKONELNVKHVKQCQETCDKLRARLVEYGFDPSRIKDLKQREDKLKSHYYQTC
                                                     AADGGYNAQLAKAKTELNEVSLAIKKSSMKMELL
                                                                   LQDYSYN-KLNNAEKD----DCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCI
                                                                                            SAKLIEKKSAYANTEK-----DYKMVQEQLSKQRDLYKRKEELVSTLTTGISSTG----
                                                                                                                  -----KLGDQATTEKGDTHIDDNKKLQEWWTIHGP--KIWEGMLCALTNGLSESEKKNI
                                                                                                                                                                                                                                                                                   172
678
1093
                                                                                                                                                                                                                                                                        1170
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                                                                                                                                                                                                                             Conservative
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I., Sasanuma M., Tsuchiya Y.,
Tashiro H., Eki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB972;
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                                                                                                                                                                                                                                                                                    1119
                                                                                                                                                                                                                                                                        133927 MW;
                                                                                                                                                                                                                                       5.7%;
22.1%;
                                                                                                                                                                                                                           50;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                 Score 97.5;
                                                                                                                                                                                                                                                                                 ALA/ASP-RICH
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                      /ASP-RICH (DA-BOX).
142B41AAE109621F CRC64;
                                                                                                                                                                                                                                        No.
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a Y., Soeda E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AT THE N- AND C-TERMINUS
                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                             118;
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                                                                                                                                                                                                                                                 Length 1170;
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Q03100;
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                                                    TRANSMEM
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                              CRANSMEM
                                                                                                                             CAMP
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HSSP; P26769; 1AB8.
DictyDb; DD02024; acaA.
InterPro; IPR001054; G_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structurally distinct and stage-specific adenylyl cyclase genes different roles in Dictyostellum development."; Cell 69:305-315(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Adenylate cyclase, aggregation specific (EC 4
                                                                                                                                                                                                                                                                                                                    Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L05497; AAA33163.1;
EMBL; L05498; AAA33163.1;
PIR; B42239; B42239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrophosphate-lyase) (Adenylyl cyclase)
ACAA OR ACA.
                                                                                                                                                                                                                                                                                  PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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  CRANSMEM
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CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.

ENZYME REGULATION: REGULATED BY A SUFFACE RECEPTOR THROUGH A

GUANINE NUCLECTIDE BINDING PROTEIN. BOTH POSITIVELY AND

NEGATIVELY REGULATED BY EXTRACELLULAR CAMP; THIS REGULATION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: CELL AGGREGATION AND LATER STAGES.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: COORDINATES CELL AGGREGATION BY SYNTHESIZING THE THAT INFLUENCES DIFFERENTIATION AND MORPHOGENESIS OF CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PART OF THE MECHANISM THAT DURING AGGREGATION.
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L05496; AAA33163.1;
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JOINED.
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Matches 69
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
                                                                                                     Presecan E., Santana M., Schneider E., Schweizer Rapoport G., Danchin A., Schneider E., Schweizer "Bacillus subtilis genome project: cloning and se kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                         MEDLINE=95020537; PubMed=7934828; Glaser P., Kunst F., Arnaud M., Coud Hullo M.F., Ionescu M., Lubochinsky
                                                                 MEDLINE=98044033; PubMed=9384377;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Protein dltD precursor.
DLTD OR IPA-2R.
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Bacteria; Firmicutes;
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15-JUN-2002
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nsky B., Marcelino L., Moszej
der E., Schweizer J., Vertes
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& Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

& Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,

& Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,

& Kurita K., Lapidus A., Lardinols S., Maubel C., Medigue C.,

& Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

& Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,

& Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

& Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

& Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescont A.M.,

& Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

& Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

& Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

& Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

& Sakiguchi J., Sekowska A., Seror S.J., Serror P., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

**Viari & Wammurt P. Wandler F. Wadler P., Wassarotti A.,

**Viari & Wammurt P., Wandenbol M., Vannier F., Vassarotti A.,
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Entian K.D., Errington J., Fabret C., Fe
Fritz C., Fujita M., Fujita Y., Fuma S.,
Ghim S.Y., Glaser P., Goffeau A., Goligh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Incorporation of D-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perego M.,
Fischer W.
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Hilbert H., Holsappel S., Hosono S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 idd in Bacillus subtilis. Identification of ge
Biol. Chem. 270:15598-15606(1995).
- FUNCTION: COULD BE RESPONSIBLE FOR THE TRAN
RESIDUES FROM D-ALA-UNDECAPRENOL PHOSPHATE
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SEKKNILQDY-SYNKLNNAEKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDV
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                                                                                                      LSELYKAMVNGQTWKVNALKPA-----AKVYYSMLEKKDLYYSTTESSGPKRYISQSV
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Guy B.J., Haga K., Haiech
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P., Minutello A.,
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Pred. No.
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5; Mismatches
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Hullo M.F., Itaya M
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Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cylicin II (Multiple-band polypeptide II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
REPEAT
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-!- FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MAY
BE INVOLVED IN SPERMATID DIFFERENTIATION.

-!- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Testis;
MEDLINE=95255491; PubMed=7737358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hess H., Heid H., Zimbelmann R., Franke W.W.; "The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II.";
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 182 KGGAKKDNKKDKKD-----
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                                                                                                   93 KIPEGFRKOMYYTFGDFRDIFFGTDISSCRYIK-DTSQTIK-----SKLGDQAT---TE 142
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                            KGDTHIDDNKKLQEWWTIHGPKIWEGMLCALTNGL----SESEKKNILQDYSYNKLNNA 197
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25 347 31 X 3 AA REPEATS OF K-K-X.
25 340 3 X APPROXIMATE TANDEM REPEATS.
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212 2.
240 3.
39079 MW; D86766599C1809E7 CRC64;
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23.8%; Pred. No. 4.2;
                                                                   KDSKKGKDIEKGKEEKLDAKKDSKKGKKDAEKGKDSATESEDE
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335 AK 336 .	305 LK 306	280 TDSDSKDDVKKESKKDATKDAKKVAKKDTEKESADSKKDAKKNAKKDAKKDAKKN	258 VKVCKEYENYITGKKTQYESQEGKFNTEKRQKKPEYNSYSKKDASEY	226 KGKDSAIELQAVKADEKKDEDGKKDANKGDESKDAKKDAKEIKKGKKDKKKPSS	198 EKDDCCLEKFASKPQFLRWYVEWSDEFCRERKKLEDKVEDVCIKAKDYEGCKNNKSNNSC

257 279 304 334

Search completed: June 20, 2003, 15:03:34 Job time: 16.5539 secs

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   1706
894
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sp_phage:*
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9.2 616 5 9.2 1210 5 9.2 1210 5 9.2 1210 5 9.2 1210 5 9.2 1270 5 9.1 177 5 8.2 2924 5 7.5 1729 5 5.7 699 5 5.6 2647 5 5.6 420 5 5.4 169 5 5.4 169 5
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# ALIGNMENTS

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Query Match
Best Local s
Matches 172
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Eukaryota; Alveolata; Apicomplexa;
MCBI_TaxID=5833;
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InterPro; IPR004258; PFEMP.
Pfam; PF03011; PFEMP; 2.
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MEDLINE=21927235;
Rowe J.A., Kyes S
                                                                                                                         Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID-5833;
                                                   SEQUENCE FROM N.A. STRAIN=TM180;
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Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=57267;
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                       PubMed=11930336;
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Last annotation updat
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                       VAR.
STRAIN-IT 4/25/5;
MEDLINE-99094502;
Smith J.D., Kyes
                                                       "Switches in the expression correlate with changes in ar infected erythrocytes."; cell 0:0-0(1995).
                                                                                                                         STRAIN=IT 4/25/5;
Smith J.D., Chitnis
                                                                                                                                                                      "The large diverse gene family var encodes proteins cytoadherence and antigenic variation of Plasmodium infected erythrocytes."; cell 82:89-100(1995).
                                                                                                                                                                                                                  Su X.Z., Heatwole V.M., Wertheimer S.P., Peterson D.S., Ravetch J.A., Wellems T.E.
                                                                                                                                                                                                                                        STRAIN=IT 4/25/5;
MEDLINE=95330813; PubMed=7606788;
                                                                                                                                                                                                                                                             [1]
SEQUENCE OF 2044-2922 FROM
                                                                                                                                                                                                                                                                                   NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                               Plasmodium falciparum Eukaryota; Alveolata;
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01-DEC-2001
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                                                                                                    Miller L.H.;
                                                                                                                                                SEQUENCE OF 2044-2922 FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Variant surface
                                                                                                                Hudson-Taylor D.E.,
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                                                                             antigenic
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 A.G.,
                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                        of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pred. No. 2.
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                                                                                                             Roberts D.
T.,
                                                                             cytoadherent
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Best Local S
Matches 122
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Q9U5M2;
01-MAY-2000
01-MAY-2000
01-MAR-2002
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SEQUENCE
                  MEDLINE-2006305; PubMed-10535993; Buffet P., Gamain B., Scheidig C., Baruch B., Oishi Fusai T., Parzy D., Miller L.H., Gysin J., Scherf A. "Plasmodium falciparum domain mediating adhesion to sulfate A: A receptor for human placental infection. Proc. Natl. Acad. Sci. U.S.A. 96:12743-12748(1999).
                                                                                                                                Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller L.H., Baruch D.I., Newbold C.I.; "Analysis of adhesive domains from the A4VAR Plasmodium falciparum erythrocyte membrane protein-1 identifies a CD36 binding domain."; wol Riochem. Parasitol. 97:133-148(1998).
                                                                                                   STRAIN-FCR3
                                                                                                            SEQUENCE FROM N.A
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Submitted (SEP-1998)
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          interPro;
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122; Conser
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IPR004258;
          IPR001219; Neurotoxin
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EMBLrel. 20,
(Fragment).
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                                                                                                                                             Apicomplexa;
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Last annotation updat
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Pred.
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No. 4.3e-35;
                                                                                                                                             Haemosporida;
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Best Local :
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Best Local Similarity
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01-JUN-2002
01-JUN-2002
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Chattopadhyay R., Pillai C.R., Chitnis C.;
Chattopadhyay R., Pillai C.R., Chitnis C.;
"Identification of a domain responsible for binding to intercellular adhesion molecule-1 from a Plasmodium falciparum field isolate.";
aubmitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV028643; AAK49742.1; -...
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NON_TER 3542 3542
SEQUENCE 3542 AA; 413089
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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              TDISSCRYIKDTSQTIKSKLGDQATTEKG-----DTHIDDNKKLQEWWTIHGPKIWEGM
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                                            EQKFKDAFIKTAAAETFLSWQYYKSKNSMDIKKLQSGEIPEEFLRSMYFTYGDYRDICLN
                                                                                        DDRTKOVGOCNAKIKNINESYPDWTCVNSKFENNEYGPCMPPRROKLCLYYLKELGENDD
                                                                                                               NDGSNEISGCNPK-----ESYPDWDC-KKNIDNSHSGACMPPRRQKLCVRDLTQGGEIRK
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TDIS--
                                                          PEDILTKFINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFG
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Alveolata;
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-KKEGD-VSDAKGKIDAYFNKYTDTNR--TKWWDTNGPEIWEGM
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Pred. No. 4.4e-33;
4; Mismatches 102
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RESULT 9
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Best Local Similarity
Matches 125; Conserv
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J. Infect. Dis. 185:1207-1211(2002).
EMBL, AJ420412; CAD20868.1; -.
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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37.3%;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
(Clone p31H) ORF (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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EMBL; Y13403; CAA73831.1; JOINED.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR004258; PFEMP.
Pfam; PF03011; PFEMP; 2.
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STRAIN-IT 4/25/5;
MEDLINE-97373957; PubMed-9230440;
MEDLINE-97373957; PubMed-9230440;
Plasmodium falciparum rosetting is me complement receptor 1.";
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Eukaryota; Alvéolata;
NCBI_TaxID=5833;
binding proteins.";
Proc. Natl. Acad. Sci. U.S.A.
PROBLE, L38454; 'AAC37240.1; -.
InterPro; IPRO04258; PFEMP.
                                                                                        MEDLINE-95350219; PubMed-7624377; Peterson D.S.; Miller L.H., Wellems T.E.; Peterson of multiple sequences from the Plasmodium Tisolation of multiple sequences from the Plasmodium that encode conserved domains homologous to those in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
NON_TER 2706 2706
                                                                                                                                                                                             STRAIN=DD2/NM;
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Pred. No. 9.3e-30;
9; Mismatches 122;
                                             92:7100-7104(1995)
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01-DEC-2001
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NON_TER
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127; Conserv
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            FGDFRDIFFGTDISSCRYIKDTSQTIKSKLGDQATTEKGDTHIDDNKKLQEWWTIHGPKI
                                         LRDAFIKSAAAETFLSWHKYKEDKKKENPTEEAPSLDVEAQTQLNDGIIPEEFKRQMFYT
                                                                                   NSDIGECIRKYKDGNEKYPVWDCTRNKIKIGEEGAYMPPRRQKLCVDFLKQLKD-QTDEK
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                                                                                                          SNEISGCNPK-----ESYPDWDCKKN-IDNSHSGACMPPRRQKLCVRDLTQGGEIRKPED
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FGDYRDLCLGKDIGNDVPIVNNNITTAFQNGAQNPSDQ----
                                                     ILTKFINCAAKETHFAWHKYKKD----
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Alveolata;
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2527
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
membrane protein 1 (Fragment).
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Pred. No. 6.6e-30;
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                                                                                                                                 Pred. No. 5e-29;
5; Mismatches 120;
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                                                                                                                                                     DB 5;
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                                                      -NVNAENELKSGKIPEGFRKQMYYT
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-DTDSQRQVFWGTYGKDI
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RESULT 12
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ID Q9U4A
AC Q9U4A
DT 01-MA
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Best Local S
Matches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97:176(
EMBL; AF193424; AAF18980.1; -
InterPro; IPR000454; Eub_ATPase_Csub
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Variant surface protein
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Eukaryota; Alveolata;
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                                               NNGLAVKEANSETYKNDPEVTEANSAKHARDYLK
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Matches 111
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01-MAY-1999
SEQUENCE FROM N.A.
MEDLINE=99021743; PubMed=9804551;
Gardner M.J., Tettelin H., Carucci
Koonin E.V., Shallom S., Mason T.,
                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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PFC112OC, MAL3P7.55.

Plasmodium falciparum (isolate 3D7).

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=36329;
                                                                                                                                            Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; "The complete nucleotide sequence of chromosome 3 of Plasmodium ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                            falciparum .";
Nature 400:532-538(1999).
EMBL; AL034559; CAB39061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO04258; PFEMP. Pfam; PF03011; PFEMP; 1. SEQUENCE 1711 AA; 196550
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EMBL; AE001366; AAC71792.1;
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33.4%; Pred. No. 3.3e-23;
Vative 49; Mismatches 110;
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	QEGKFNTEKRQKKPEY  : :  ::  :   CKSAYNEQKTKY	IKAK     ENTGARGGTTKQKYSO	KASTASQTPSPRASGE	GMLCALT NGLSESE   :     :    GMIYALTYDTNTASGE	IKDTSQTIKSKLGDQA :  :       LKASGDNPTNKLTIQO	NAE  -   GNGGVAQFFGSYSGSE	STSPQPGESGVANASA	TGSTTKQNDSEGSEGG	52; Mismatches
	ENGNN	DYEGCI	NKPTT	KKIEKI	TTEK-	SEEKT	SSTSSI	HRSKRI	116;
	K       KGGGGNGV	KNNKSNN-     SKIVENKD	LEKFASKP  :   :  LDSFVKRP	DDAVYKKLI	KNVIEKSGI	NAENELKSGKIPEGFRKOMYY : :     :         :  :   SYSGSESEEKTPQQWLQSGTIPTDFLRQMFY	PEDII 	KKNIDNSHSGACMPPR  :: ::       :    GGHRSKRHTESSDSTTTSSGSVCVPPR	Indels
	CGTLQE	KIFKDI	QFLRWY :  : TYFRYI	WDEANN	DT      DTPSRT	KIPEGE       IPTDE	LTKEIN    RDAFIQ	G	189;
	DASEYL     : : :     GVCGTLQENAADFL	EKPSCA	VEWSDE	KPKKDN	THI	RKQMYY :  :  LRQMFY	CAAKET	ACMPPR  :    VCVPPR	Gaps
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Novel FCR3.varCSA protein, useful for modulating parasitized red becall binding, sequestration and onset of maternal malaria	WPI; 2001-235109/24.	Gysin J, Pouvelle B, Fujii N, Smith J;	Gamain B,	(USSH ) US DEPT HEALTH & HUMAN SERVICES.		01-SEP-1999; 99US-0152023.	01-SEP-2000; 2000WO-US24195.		08-MAR-2001.		WO200116326-A2.					membrane protein 1; parasitized	FCR3.varCSA protein; chondroitin sulfate A; CSA; var gene; PFEMP1;		P. falciparum varCSA polypeptide A4tresDBL3-gamma.	29-MAY-2001 (first entry)		AAB62149;		2149 AAB62149 standard; peptide; 351 AA.	

Novel FCR3.varCSA protein, useful for modulating parasitized red blood cell binding, sequestration and onset of maternal malaria -  $\,$ 

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                   Chitnis C, Mill
Wellems TE;
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                                                                            (USSH ) US THEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICTNG
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                                               Miller
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                                                                                                                                                                                                                                                                              binding ligand; E31a; binding domain; malaria; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                  E31a
                                                                                                           93US-0119677.
                                                                                                                                         94WO-US10230
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                                               LH,
                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                               Peterson
                                                                                                                                                                                                                                                                                                                                                                                                               793
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Pred. No. 3.6e-167;
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Best Local
                                                                                                       DBL gene family; SABP; sialic acid binding protein; vaccine; Duffy binding like gene; Duffy antigen binding protein; erytl DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erythrocyte binding ligand (EBL) family genes were clop. Falciparum chromosome 7 subsegment libraries construgenetic studies of the chloroguine resistance locus. EBL-e1 (AAQ83526), E31a (AAQ83527), EBL-e2 (AAQ83528)
                                                                  Plasmodium falciparum
                                                                                              Plasmodium
                                                                                                                                                                  Plasmodium
                                                                                                                                                                                               07-OCT-1997
                                                                                                                                                                                                                                                      AAW22480 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAQ83529), encode the proteins given in AAR70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, mammalian, insect, and in vaccinia virus and adenovirus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New erythrocyte binding domain polypeptide(s) - isolated i 
Plasmodium binding proteins, used in diagnosis, treatment 
prevention of malaria
                                       W09640766-A2
                                                                                                                                                                                                                           AAW22480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWKGMLCALSYNT-----ET-KKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGDYRDICLDTDI-SEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMTNTNE---LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEIVAEMLKUKNGRTTVGECYRKETYSEWTCDESKIKMGQ-HGACIPPRRQKLCLHYLEK
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                                                                                                                                                                   E31a
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Pred. No. 2.9e-50;
4; Mismatches 112
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.Wellems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the buffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see AMT72889 and AAMT72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially Plasmodium falciparum or Plasmodium vivax).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compositions are used for the treatment and prevention of malaria, y are also used in the preparation of vaccines for inducing a tective immune response in a mammal to Plasmodium merozoites
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DB; AAT72895.
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                                                                                                                                                                                                                                                                                                                                        LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT 1.14
                                                                                                                                           FGDYRDICLDTDI-SEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS
                                                                                                                                                                                                                                                                                                                       IMTNTNE--LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                    CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENT--KLGEDEGVCMPPRRQNLCVHYLTK
MKCVNG
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                                                            WIDNYKKQKGRYTEVK
                                                                                           WKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLEN
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41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        culture supernatant after erythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protozoacide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBL gene; Duffy-binding DABP; Sialic Acid Bindir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. falciparum ebl-1 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY77902 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the buffy and start after some soluble proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Local 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be d to vaccinate against malaria, especially caused by P. falciparum. unization with the polypeptide provides effective protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-194198/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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VTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMER
                                                                                                                                                                                                                                                                    IMTNTNE---LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein binding domains from Plasmodium vivax and Plasmodium userythrocyte binding proteins useful for vaccinating agains
                                                                                                                      IWKGMLCALSYNT----
                                                                                                                                                                      FADYRDICLGTDISSKKDTSKGVGKVKCNIDDVFYKISN-----SIRYRKSWWETNGPV
                                                                                                                                                                                                               FGDYRDICLDTDI-SEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS
                                                                                                                                                                                                                                                                                                LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT
                                                                                                                                                                                                                                                                                                                                                                    CEIVAEMLKDKNGRTTVGECYRKETYSEWTCDESKIKMGQ-HGACIPPRRQKLCLHYLEK
                                                                                                                                                                                                                                                                                                                                                                                                                 CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENT--KLGEDEGVCMPPRRQNLCVHYLTK
                                                                         IWEGMLCALSYDTSLNNVNPETHKKLTEGNNNF-EKVIF-GSDSSTTLSKFSERPQFLRW
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ng Protein;
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                                                                                                                      -ET-KKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DS,
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SABP; m
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                                                                                                                                                                                                                                   Erythrocyte binding ligand (EBL) family genes were cloned from P. falciparum chromosome 7 subsegment libraries constructed during genetic studies of the chloroquine resistance locus. The 4 genes, EBL-e1 (AAQ83526), E31a (AAQ83527), EBL-e2 (AAQ83528) and Proj3 (AAQ83529), encode the proteins given in AAR70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, mammalian, insect, and in vaccinia virus and denovirus-infected cells, and provide protection against P. falciparum.
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 61-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitnis C,
Wellems TE;
                                                                                                                                                                                                                                                                                                                                                                                               New erythrocyte binding domain polypeptide(s) - Plasmodium binding proteins, used in diagnosis, prevention of malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-123427/16.
N-PSDB; AAQ83529.
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mes 137; Conser
                                        1402 QTENIKTDDNLKDAFIKTAAAETFLSWQYYKSKNDSEAKILDRGLIPSQFLRSMMYTFGD
                                                                                                       1342
118 YRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSTWKG
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                                                                                                                        2 CKMYQKLISEQIEKNNIHNCKKTED-AKWKCENTKLGEDEGVCMPPRRQNLCVHYL---T 57
                                                       KLNDDSKEEDLREAFIKSAAAETFILRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD 117
                                                                                              CKIVEKILEGKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHES 1401
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                                                                                                                                                                                                                2703 AA;
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                                                                                                                                                                        32.7%;
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                                                                                                                                                         61;
                                                                                                                                                        Score 625.5; I
Pred. No. 1.3e
51; Mismatchės
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                                                                                                                                                                         1.3e-47;
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                                                                                                                                                                                     DB 16;
                                                                                                                                                         126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; malaria; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Su
                                                                                                                                                                                                                                                                                                                                                                                                       isolated from treatment and
                                                                                                                                                        Indels
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                                                                                                                                                                                  Length
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falciparum or Plasmodium

a mammal

to Plasmodium merozoites

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RESULT 6
AAW22482
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                   This sequence represents Proj3 of Plasmodium. Proj3 belongs to CC the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein CC (SABP) conserved regions (see AAT72889 and AAT72888 respectively). The CC Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte supernatant. The sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DaBP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a conservative immune response in a mammal to placed in the correction.
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                                                                                                                                                                                                                                                                                                                                           Disclosure;
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Wellems TE;
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                                                                                                                                                                                                                                                                                                                                                                             binding
                                                                                                                                                                                                                                                                                                                                                                                                             New malaria vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DBL gene family; SABP; sialic acid binding protein; vaccine; therapy; Duffy binding like gene; Duffy antigen binding protein; erythrocyte; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US
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Best Local
The invention relates to ebl-1 polypeptides that are encoded by the DBI (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the
                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                      US5993827-A
                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                             DBL gene; Duffy-binding like gene; DABP; Sialic Acid Binding Protein;
                                                                                                                                                                                                                                                                                                                                                                                P. falciparum Proj3 binding domain polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                              Disclosure;
                                                                                            Isolated protein binding domains from Plasmodium vivax and Plasmodium falciparum erythrocyte binding proteins useful for vaccinating agains
                                                                                                                                                                                         (USSH)
                                                                                                                                                                                                                10-SEP-1993;
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                                                          Columns 79-92; 93pp; English
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Pred. No. 1.3e-47;
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SABP; malaria; vaccine; immunisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              culture supernatant after erythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against malaria. The present sequence represents the Proj3 binding domain
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137; Conserv
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                                                                                                                                           MLCALTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAE
                                                                                                                                                             MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKN
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                                                                                                                                                                                                                                 YRDICLDTDISEKIADHDYTTAKKKITAVFQKIGSKTINGKKVLEREGWWKEYGLSIWKG
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                                                                                                                                                                                                                                                                                                       KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD
FVLKANVQPQD-----PEYKGYEYKDGVQPIQGN----
                                  FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT
                                                                   ROKKENIIKDAC-----NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN
                                                                                                    RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 625.5; DB 21;
Pred. No. 1.3e-47;
1; Mismatches 126;
 -EYLLQKCDNNKCS
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#### AAW22475 ID AAW ACCOMMON ACC 12-SEP-1997 Plasmodium var-7 AAW22475; AAW22475

(first entry)

RESULT

standard;

Protein;

3060

A

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy; Duffy binding like gene; Duffy antigen binding protein; erythrocyte; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response Plasmodium response;

Plasmodium Plasmodium vivax. falciparum

19-DEC-1996.

W09640766-A2

07-JUN-1996; 96WO-US09508

07-JUN-1995; 95US-0487826

S HEALTH & HUMAN SERVICES

Chitnis Wellems TE; Miller LH, Peterson DS, Sim ŽĽ, Su ×

WPI; N-PSDB; AAT72882 1997-052231/05

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                               DBL gene; Duffy-binding like gene; DABP; Sialic Acid Binding Protein; protozoacide; var-7.
Plasmodium sp
                                                                                                  Plasmodium var-7 polypeptide
                                                                                                                                           13-JUN-2000
                                                                                                                                                                                                            AAY77905 standard;
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binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKN
                                                                                                                                                                                                                                                                                                                                                                                                            237
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                                                                                                                                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Page 61-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                    MLCALTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains homologous proteins
                                                                                                                                                                                                                                                                                                    FVLKANVQPQD---
                                                                                                                                                                                                                                                                                                                              FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT 349
                                                                                                                                                                                                                                                                                                                                                                 RQKKENIIKDAC-----NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN
                                                                                                                                                                                                                                                                                                                                                                                                 RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRDICLNTDISKK--QNDVAKAKDKIGKFFSKDGSKSPSG---LSRQEWWKTNGPEIWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLERBGWWKEYGLSIWKG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTENIKTDDNLKDAFIKTAAAETFLSWQYYKSKNDSEAKILDRGLIPSQFLRSMMYTFGD 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKIVEKILEGKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHES
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                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contains cysteine-rich DBL family protein yous domains of the Duffy and sialic acid
                                                                                                                                                                                                                                                                                              -PEYKGYEYKDGVQPIQGN-----EYLLQKCDNNKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 625.5; DB 18;
; Pred. No. 1.5e-47;
61; Mismatches 126;
                                                                                                                                                                                                              3060
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                                                                                                                                                                                                            A
                                                ebl-1;
SABP; π
                                              malaria;
                                                           Duffy Antigen Binding Protein;
                                              vaccine;
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                                            immunisation;
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RESULT 10 AAB62142

AAB62142 standard;

Protein;

3542

AA

29-MAY-2001 AAB62142;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to ebl-1 polypeptides that are encoded by the DBL (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the culture supernatant after crythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and Sialic acid receptors on crythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against malaria. The present sequence represents the var-7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated protein binding domains from Plasmodium vivax and Plasmodium falciparum erythrocyte binding proteins useful for vaccinating agains
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                                                                                                                                      178 MICALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKN
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                                    297
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FVLKANVQPQD----PEYKGYEYKDGVQPIQGN---
                                                                                                                                                                                                   YRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKG
                              FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT
                                                                                        RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK
                                                                                                                      {\tt MLCALTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAE}
                                                                                                                                                                                 YRDICLNTDISKK--QNDVAKAKDKIGKFFSKDGSKSPSG---LSRQEWWKTNGPEIWKG
                                                                                                                                                                                                                                                            CKIVEKILEGKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHES
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3060 AA;
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38.8%;
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                                                                                                                                                                                                                                                                                                                                                                     61;
                                                            NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN
                                                                                                                                                                                                                                                                                                                                                                      Score 625.5; DB 2
Pred. No. 1.5e-47;
1; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                      126;
 -EYLLQKCDNNKCS
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AAB62148
ID AAB6
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                                                                         RESULT 11
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Best Local
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Gysin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondroitin sulfate A (CSA). The var gene and the corresponding P. falciparum erythrocyte membrane protein 1 (PERMP1) modulate adhesion of parasitized red blood cell (PRBC) to CSA. The protein and the encoding gene are useful for treating and preventing maternal malaria in a patient identified at a risk for contracting maternal malaria or in a patient afflicted with maternal malaria. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel FCR3.varCSA protein, useful for modulating parasitized cell binding, sequestration and onset of maternal malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FCR3.varCSA protein; erythrocyte membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1999;
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                           AAB62148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents the P. falciparum FCR3.varCSA protein
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                         standard;
                                                                                                                                                                                                                                            WYDDYCYTROKYLKDVQEKCKS
                                                                                                                                                                                                                                                                   WGEDFYKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGA-CKTQCEKYKKWMERWK 287
                                                                                                                                                                                                                                                                                                                                            HEIWEAMLCAL-VKIGAKKDD----
                                                                                                                                                                                                                                                                                                                                                                   LSIWKGMLCALSYNTETKKMDEGVRTYLMKYIYKN---NDIKEYLEEFASRPPFLRWVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                    FYTFGDYRDFLFGTDISK--GHGEGSKLKEQIDSLFKNGDQKSPNGK---TRQEWWTEHS
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                                                                                                                                               KEWIPQDKYYKDERDKKRFDRQHIGVMVTDYTGTNATDYLN
                                                                                                                                                                                            KHYSSQKKKFQLYKNSATYNN---GLAVKE---ANSETYKN 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 63-71; 78pp; English.
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Pouvelle B,
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                      peptide;
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protein 1; parasitized
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Fujii N,
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                      407
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Pred. No. 1.5e-40;
8; Mismatches 115;
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Smith J;
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red blood cell; PRBC;
                                                                                                                                                                                                                                          NDQLKCDTECNKKCEDYVKYMKK-K 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a P. falciparum FCR3 varCSA protein, that is capable of binding to chondroitin sulfatte A (CSA). The var gene and the corresponding P. falciparum erythrocyte membrane protein 1 (PFERP1) modulate adhesion of parasitized red blood cell (PRBC) to CSA. The
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A4 DBL4-gamma.
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erythrocyte membrane protein 1; protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel FCR3.varCSA protein, useful for modulating parasitized cell binding, sequestration and onset of maternal malaria -
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348
                                        285 DQYEQQTAKFD
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126; Conserv
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CTNG
                                                                                          KHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMI
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                                                                                                                                                                                                                                       DIWKGMYCGLSHH-----IKNGNKEQLRKNLTDNNKYTKISSKLEDFASRPQFLRWFIEW
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                                                                                                                                             GDQFCRERVVKINQLKTGCNEYECGSQENGKKE-
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Fujii N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 548; DB 22;
Pred. No. 1.1e-41;
2; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baruch I
Smith J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A4 DBL4-gamma
                                          -KDKKDKKFDGTSAEVDVAAVSSVHEYLQEELKN-L
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                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        Scherf A,
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R29DBL2-gamma.
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VTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMER
                                                                                                KNKYQLREAFIKCAAKETNLLWDKYKNDKN-EAEELLKKGKIPEDFMRIMFYTFGDFRDF 116
                                                                                                              SKEEDLREAFIKSAAAETFLL-RQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDI 121
                                                                                                                                        VLQQKSNGSIDNCNAKNRKKNE----WQCDKNTFVDGNEGVCMPPRRKSICIHNLTLEEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protozoacide;
                   L-IHADTKDS------IKNKDNYKYEKVTILAKRDGSNGMTLSEFAKKPKFLRW
                                       LSYNTETKKMDEGVRTYLMKYIYKNNDIKEY--
                                                           CLENDMGK----
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Pouvelle B,
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                                                                                                                                                                                                                     294 AA;
                                                                                                                                                                                                                                                                                                                                           Page 72;
                                                                                                                                                                              Conservative
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                                                                                                                                                                                       Score 509.5; DB 2
Pred. No. 2.4e-38;
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of binding to chondroitin sulfate A (CSA). The var gene and the corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1) modulate adhesion of parasitized red blood cell (PRBC) to CSA. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 54; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel FCR3.varCSA protein, useful for cell binding, sequestration and onset
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FVEWYDDYCKERQKYLTEVASTCKSI---
                                                                   DVT-TAKKKI--TAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCALSYN-TETKK
                                                                                                      CAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRDIFFGTDISSCRYIK
                                                                                                                                       SAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISEKIADH
                                  DTSQTIKSKLGDQATTEKGDTHIDDNKKLQE--
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MDEGVRTYLMKYIYK -- NNDIKE--YLEEFASRPPFLRWVTEWGEDFVKNRKKELVSLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ItG2-CS2 DBL2..
                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
                                                                                                                                                                                                                                            Score 444; DB 22;
Pred. No. 2.7e-32;
6; Mismatches 131;
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parasitized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baruch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulating parasitized of maternal malaria -
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                                  WWTIHGPKIWEGMLCALTNGLSESEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFEMP1;
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RESULT 14
AAB62150
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                                                                                                                                                                                                                     maternal malaria in a patient identified at a risk for contracting maternal malaria or in a patient afflicted with maternal malaria. The present sequence represents a P. falciparum varCSA polypeptide FCR3 var3DBL-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scherf A,
Gysin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCR3.varCSA protein; chondroitin sulfate A; erythrocyte membrane protein 1; parasitized malaria; protozoacide; FCR3 var3DBL-gamma.
                                                                                                                                                                                                                                                                                 The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondrolitin sulfate A (CSA). The var gene and the corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1) modulate adhesion of parasitized red blood cell (PREC) to CSA. The protein and the encoding gene are useful for treating and preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Novel FCR3.varCSA protein, useful for modulating parasitized cell binding, sequestration and onset of maternal malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000WO-US24195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB62150 standard;
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 74-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                          IRTEFIKSAAIETHFAWDRYKEDNGEAEAELKNGNIPEGFKROMYYTFGDYRDIFFGRDI
                                                      LREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDI
                                                                                ETDDIDGCNQKYKAGKDKYPGWDCNSQIHTTHNGACMPPRRQKLCVSGLTKTDRIKAIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller LH, Pouvelle B,
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                                                                                                                                          Conservative
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-- EKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCAL
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Fujii N,
                                                                                                                                                                                                                                                                                                                                                                   78pp;
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                                                                                                                                                    Score 440; DB 22;
Pred. No. 6.3e-32;
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Smith J;
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blood cell; PRBC;
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RESULT 15
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                                                         New Plasmodium falciparum erythrocyte membrane develop products for the diagnosis, treatment of malaria parasite infections
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                                     Claim 1; Figure 12; 149pp; English.
                                                                                                   N-PSDB;
                                                                                                           WPI; 1996-497376/49
                                                                                                                                Baruch DI,
                                                                                                                                                                                             26-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification;
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                                                                                                                                Howard RJ,
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/note= "Cysteine rich
839..1272
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                                                                                                                                                                                                                                                                                                /label= Duffy binding
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                                                                                                                                                                                                                                                                                                                                         /note= "Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                    /label= Duffy binding
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           'label Duffy binding ligand
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                                                                                                                                                                                                                                                                             "Cysteine
                                                                                                                                Pasloske
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prevention
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on of
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A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a

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Search completed: June 20, 2003, 15:02:55 Job time: 59.4583 secs
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Best Local Similarity 26.3
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMPI polypeptide or its fragments may be used in diagnosis of malaria infection. This is the PfEMPI protein of the MC type of Plasmodium falciparum. An alternative, truncated pfEMPI protein is given in AAW00385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LKKKCDSCTLRNNGTSNKTC---
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                                                                                                                          --ELKHCKNG 1303
                                                                                                                                                                                                                                                                                                               KKHYSSQKKKFQ-----LYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKT 341
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                                                                                                                                                                                                                                                                                                                                                                                                            ---DDNE-----NCGACKTQCEKYKKWMERW 286
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Result
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1913
1 PCKMVQKLISEQIE
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1: /ggn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 1008
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                                        1435
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US-08-487-825B-16
US-08-487-825B-6
US-08-487-826B-6
US-08-487-826B-6
US-08-487-825B-4
US-08-487-825B-4
US-09-210-288-4
US-09-210-288-1
US-09-210-288-17
US-08-487-825B-29
US-09-210-288-17
US-08-487-825B-2
US-08-487-825B-2
US-08-487-825B-2
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US-08-568-459A-12
US-08-487-826B-12
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                                 Sequence 4, Appli
Sequence 17, Appl
Sequence 27, Appl
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Sequence 33, Appl
Sequence 21, Appl
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107	131.5	131.5	131.5	135	135	135	137	137	137	144.5	144.5	144.5	167	171	171	171	171.5
5.6	6.9	6.9	6.9	7.1	7.1	7.1	7.2	7.2	7.2	7.6	7.6	7.6	8.7	8.9	8.9	8.9	9.0
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US-08-929-329-5	US-09-210-288-18	US-08-487-826B-30	US-08-568-459A-18	US-09-210-288-13	US-08-487-826B-25	US-08-568-459A-13	US-09-210-288-16	US-08-487-826B-28	US-08-568-459A-16	US-09-210-288-20	US-08-487-826B-32	US-08-568-459A-20	5198347-2	US-09-210-288-15	US-08-487-826B-27	US-08-568-459A-15	5198347-4
	-	Sequence 30, Appl	-	-	-	-	Sequence 16, Appl	`	`	•	•	•	Patent No. 5198347	Sequence 15, Appl	Sequence 27, Appl	•	Patent No. 5198347

## ALIGNMENTS

RESULT 1 US-08-568-459A-8

Sequence 8, Application Patent No. 5849306 GENERAL INFORMATION:

Application US/08568459A

APPLICANT:
APPLICANT:
APPLICANT:

Sim, Kim L.
Chitnis, Chetan
Chiller, Louis H.
Miller, Louis H.
Peterson, David S

```
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSED, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHI
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 235-8550
TELECHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 620 nc., STREET: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
ORIGINAL SOURCE: ORGANISM: Pla
                                       MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                LENGTH: 921 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                   TOPOLOGY:
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                                                                                                                                          921 amino acids
Plasmodium falciparum
                                                                                   linear
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Query Match

33.8%;

Score 646;

DB 2;

Length 921;

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286 WKKHYSSOKKKFQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTOLEN 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 IMTNINE--LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 CEIVAEMLKDKNGRTTVGECYRKETYSEWTCDESKIKMGQ-HGACIPPRRQKLCLHYLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 INDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT 114 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Knobbe Martens Olson & Bear T: 620 Newport Center Drive 16th Floor Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWEGMLCALSYDTSLNNVNPETHKKLTEGNNNF-EKVIF-GSDSSTTLSKFSERPQFLRW 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWKGMLCALSYNT-----ET-KKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FADYRDICLGTDISSKKDTSKGVGKVKCNIDDVFYKISN-----SIRYRKSWWETNGPV 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                NIH121.001CP1
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                                                                                                                                                                                                                                                                                                   Version #1.25
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US-09-210-288-8
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 150;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              FILING DATE:
                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                 COUNTRY: U.ZIP: 92660
                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENT--KLGEDEGVCMPPRRQNLCVHYLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTEWGEDFVKNRKKELVSLKKKODSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGDYRDICLDTDI-SEKIADHDYTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMTNTNE--LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09210288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWEGMLCALSYDTSLNNVNPETHKKLTEGNNNF-EKVIF-GSDSSTTLSKFSERPQFLRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sim, Kim L.
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                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 646; DB 2;
Pred. No. 2.4e-50;
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                                                                                                                                                                                                                                                                                         16th Floor
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174

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Matches

Local Similarity

Conservative

41.0%;

Pred.

. No. 2.4e-50;

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RESULT 2 US-08-487-826B-8

Patent No. Sequence

8, 55, 127 No. 5993827

Application US/08487826B

GENERAL INFORMATION:

APPLICANT: Sim, Kim
APPLICANT: Chitnis,
APPLICANT: Miller, i)
APPLICANT: Peterson
APPLICANT: Su, xin:
APPLICANT: Wellems,

Peterson, David S. Su, Xin-zhaun
Wellems, Thomas E. Chitnis, Chetan Miller, Louis H. Sim, Kim L.

CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES:

STREET: ADDRESSEE:

INFORMATION FOR SEQ ID NO:

(619)

235-0176 235-8550

8:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550

TELEPHONE:

REFERENCE/DOCKET NUMBER:

REGISTRATION NUMBER:

29,655

ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned

Israelsen, Ned

FILING DATE: 10 CLASSIFICATION:

10-SEP-1993 N: 435

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY:

California

92660

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

PatentIn Release #1.0,

SOFTWARE:

APPLICATION NUMBER: US/08/487,826B

SEQUENCE CHARACTERISTICS: LENGTH: 921 amino acid

amino acid

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                                                                                                                                                                                                                                                                                             Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                     APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
NUMBER OF SEQÜENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: NII
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                             APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                      CORRESPONDENCE ADDRESS:
                                COUNTRY: U
ZIP: 92660
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TOPOLOGY: li
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                                                              STATE:
                                                                                         STREET:
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                                                                            Newport Beach
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                                                            California
                                                                                                                                                                                                                                                                                                           Application US/08568459A
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                                                                                         E: Knobbe Martens Olson & 620 Newport Center Drive
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Floppy disk
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Pred. No. 2.4e-50;
                                                                                         Floor
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                                                                                                                                                                                                                Patent No.
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Best Local
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                                                                                                                                                                                 APPLICANT:
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TOPOLOGY: li
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Sequence 12, Application Patent No. 5993827
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TELEFAX: (617) ...
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
2710 amino acids
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                    APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Meterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: pr
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ATTORNEY/AGENT INFORMATION:
                                                                      CORRESPONDENCE ADDRESS
                                                                                               NUMBER OF SEQUENCES:
  ADDRESSEE: KILLER BOOKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 07-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1524 MLCALTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAE 158:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CKMYQKLISEQIEKNNIHNCKKTED-AKWKCENTKLGEDEGVCMPPRRQNLCVHYL---T 57
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVLKANVQPQD-----PEYKGYEYKDGVQPIQGN-----EYLLQKCDNNKCS 1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQKKENIIKDAC-----NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN 1635
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                                             Knobbe Martens Olson &
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                                                                                                                                                                                                                                                                                      Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.7%; Score 625.5; DB 2; 38.8%; Pred. No. 8.1e-48; tive 61; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                              US/08487826B
                         Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/568,459A
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                         Bear
16th
                      Floor
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                                                                                                                     BINDING
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RESULT 6
US-09-210-288-12
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                                                                                                                                             Patent No. GENERAL I
                                                                                                                                                                            Sequence
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                                                                  APPLICANT:
                                   TITLE OF INVENTION:
                    FITLE OF INVENTION:
                                                     APPLICANT:
                                                                                                  APPLICANT:
                                                                                                               APPLICANT:
                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                                                                             FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT 349
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                                                                                                                                                                                                                                                                                                          RQKKENIIKDAC-----NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN 1635
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                                                                                                                                                                         Application US/09210288
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                                                                           Miller, Louis H
Peterson, David S.
                                                 Wellems,
                                                                                                          Chitnis, Chetan
                                                                                                                             Sim, Kim L.
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                                                Thomas E.
                BINDING DOMAINS FROM PLASM AND PLASMODIUM FALCIPARUM
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            DOMAINS FROM PLASMODIUM VIVAX
SMODIUM FALCIPARUM ERYTHROCYTE BINDING
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Pred. No. 8.1e-48;
1; Mismatches 126
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US-08-487-826B-14
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                                                     Sequence 14, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
                      APPLICANT:
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Sim, Kim L. Chitnis, Chetan Miller, Louis H.

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US-09-210-288-12
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Matches 137;
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MOLECULE TYPE: pr
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasm
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CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version.#1.25
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CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fuller, Michael REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                   FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT 349
FVLKANVQPQD-----PEYKGYEYKDGVQPIQGN--
                                                                                                          RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK 296
                                                                                                                                                    MLCALTKYVTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRMMIEWGEEFCAE
                                                                                                                                                                                     MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKN 236
                                                                                                                                                                                                                                                                                                                                        KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD
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38.8%;
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                                                                         NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN 1635
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   -EYLLQKCDNNKCS
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Sequence 16, Application US/08487826B Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 137;
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
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TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: California
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                                                                                                                                                        FVLKANVQPQD-----PEYKGYEYKDGVQPIQGN-----EYLLQKCDNNKCS 1675
                                                                                                                                                                                            FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT 349
                                                                                                                                                                                                                                   RQKKENIIKDAC-----NEINSTQQCNDAKH--RCNQACRAYQEYVENKKKEFSGQTNN
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Pred. No. 9.7e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US/08/487,826B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM:
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                               1142 ANKNTPIEKYQYTNYKLEDESGAKSNDTIQPPTLKNEVEIPTEFRWLHEWGNSECFERAK 120:
                                                                                                                                                                            1029 NDTSD-----TTGKQTPSSSNDNLKNIVLEASGSTEQEKEKMKQIQAKIKKILNGATS 1081
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240 ELVSLKKKCDSCTLRNNGTSNKTCDDNENC------GACKTQCEKYKKWME 284
                                                                                                                                                                                                                                                                                                                       909 RRRLYVGGLSQWASRGGDETTEVSSEATSAPSQSESEKLRTAFIESAAIETFFLWHKYKE 968
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                                                                                                       GVPPVTKNSVKTPQQTWWENIAKDIWNAMVCALTYKENDARGTSAKIEQNKDLKKALWDE 1141
                                                                                                                                         GKKVLER-----EGWWKEYGLSIWKGMLCALSY-----NTETKK--MDE 193
                                                                                                                                                                                                                                                                                        KNV
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Miller, Louis
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Wellems, Thom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                  -KNNDIKE--YLEEFASRPPFLRWVTEWGEDFVKNRKK 239
                                                                                                                                                                                                                                                                       TKLNDDSKEEDLREAFIKSAAAETFLLRQYYNS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                 ----KKITAVFQKIGSKTTN 156
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US-08-568-459A-6

Sequence Patent No.

APPLICANT:

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GENERAL INFORMATION:
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LENGTH: 749 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                            126 DISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVL----EREGWWKEYGLSIWKGMLCA 181
182 LSYNTETKKMDEGVRTYLMKYTYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKNRKKEL
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T: 620 Newport Center Drive 16th Floor
Newport Beach
                              DVW----RDINT--NKLSEKFQKIFMGGGNSRKKQNDNNERNKWWEKQRNLIWSSM---
                                                                                             EGLKDHINKAANYEAMHLKEKY--ENAGGDKICN-----AILGSYADIGDIVRGL
                                                                                                                           EDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDT 125
                                                                                                                                                           SKEHEESSVFGCKTKISKVKKKWNCYSNNKVTKPEGVCGPPRRQQLCLGYIFLIR-DGNE
                                                                                                                                                                                        SEQIEKNNIHNCK---KTEDAKWKC-ENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDSKE
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                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
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AND PLASMODIUM
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                                                                                                                                                                                                                                             Score 353; DB 2;
Pred. No. 8.9e-24;
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SMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                Mismatches 118;
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US-08-487-826B-6
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Matches
                                                                             Query Match
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                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: pro
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                                                                                                                                                                       HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 10-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM. PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
COMPUTER: II
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      10 SEQIEKNNIHNCK---KTEDAKWKC-ENTKLGEDEGVCMPPRRONLCVHYLTKLNDDSKE 65
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o. 5993827
                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   Israelsen, Ned
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                                                                                                                                                                                                                                                                   749 amino acids
                                                                                                                                                                                                                                                                                                                       (619)
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Wellems, Thomas E.
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Miller, Louis H.
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                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                    235-0176
                                                                      18.5%; Score 353; DB 2; 28.2%; Pred. No. 8.9e-24; tive 50; Mismatches 118;
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16th Floor
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                                                                                                      Length 749;
                                                                      Indels
                                                                      94;
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US-08-568-459A-6

ORGANISM:

HYPOTHETICAL: I ORIGINAL SOURCE:

STRANDEDNESS:

TELEPHONE:

SOFTWARE:

COUNTRY:

92660

STREET: ADDRESSEE:

Matches Query Match

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US-09-210-288-6
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ORGANISM:
-09-210-288-6
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                                                                                                                              TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 amino acid
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                 ORIGINAL SOURCE
                                              HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     NAME: Fuller, Michael REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                 TOPOLOGY:
                                                                                                STRANDEDNESS:
                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Knobbe Martens Olson & 620 Newport Center Drive
                                                                                                                              749 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller, Louis H.
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Chitnis, Chetan
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                                                                              ss: single
linear
                Plasmodium falciparum
                                                                                                                                                                                                     (619)
                                                                protein
                                                                                                                                                                                 235-0176
                                                                                                                                                                                                   235-8550
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16th
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US-08-568-459A-4
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Best Local Similarity
Matches 103; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5849306 GENERAL INFORMATION:
    INFORMATION FOR
                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                 NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                             FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                             COMPUTER:
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                                                                   REFERENCE/DOCKET NUMBER:
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                                  TELEPHONE:
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T: 620 Newport Center Drive 16th
Newport Beach
California
                                                                                                                                                                                                                                                                             92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08568459A
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                     (619)
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Wellems, Thomas E.
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Miller, Louis H.
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                                                                                                                                                                                                           IBM PC compatible SYSTEM: PC-DOS/MS-DOS
    SEQ ID NO:
                                  (619)
9) 232
, 235-0176
, 200: 4:
                                                                                                                                                                                                                                                                                                                                                                                      BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE: 37
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28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chetan
                                                                                                                                                                                           Release #1.0, Version
                                                                                                                                                             US/08/568,459A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KFEDSKAYLRSESKQCSNIEFNDETFTFPNKYKEA------C
                                                                                 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 353; DB 4;
Pred. No. 8.9e-24;
50; Mismatches 118
                                                                  NIH121.001CP1
                                                                                                                                                                                                                                                                                                                                      16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CKNACSSYEKWIKERKNEYNLQSKKFDSDK
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                                                                                                                                                                                              #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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US-08-487-826B-4
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APPLICANT: Sim, K
                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                      APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993
                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                 NAME: Israelsen, Ne
REGISTRATION NUMBER:
                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 87; Conserv
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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California
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Miller, Louis H.
                                                                                                                                                                                                                                                                                                                 620 Newport Center Drive
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Su, Xin-zhaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              David S.
                 29,655
NIH121.001CP1
                                                                                                                                                Version #1
                                                                                                                                                                                                                                                                                                                 16th Floor
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RESULT 14
US-09-210-288-4
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIJUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  APPLICANT: Wellems, Thomas E. APPLICANT: Wellems, Thomas E. TITLE OF INVENTION: BIDDING DTITLE OF INVENTION: AND PLASM
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                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                 CITY: Newport Beach
STATE: California
                                                                                                                 COUNTRY:
                                                                                                                                                                     STREET:
                                                                                                                                                                                   ADDRESSEE:
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                                                                                                     92660
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                                                                                                                                                                     620 Newport Center Drive
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Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                      Sim, Kim L.
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linear
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Newbort Center Drive 16th Floor
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235-0176
ID NO: 4:
                                                                                                                                                                                                                      AND PLASMODIUM: 37
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                                                                                                                                                                                                                                  DOMAINS FROM PLASMODIUM VIVAX
SMODIUM FALCIPARUM ERYTHROCYTE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 329; DB 2; Pred. No. 3.4e-21;
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                   #1.25
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APPLICATION NUMBER:

US/09/210,288

ATTORNEY/AGENT INFORMATION: NAME: Fuller, Michael

Fuller, Michael

CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                            Patent No. 5849306
                                                                                                                                                                                                                                                                                                                                                                               08-568-459A-17
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        THE OF INVENTION:
                                                                   COUNTRY:
                                                                                        STATE:
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STRANDEDNESS: si
                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 LSYNTETKKMDEGVRTYLMKYIYKNNDI-KEYLEEFASRPPFLRWVTEWGEDFVKNRKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 KNSATYNNGLAVKEANSETY--KNDPEVTEANSAKHARDYLKTQLENMICT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 DKNSV----DTNTKVWECKNPYILSTKDVCVPPRRQELCLGNIDRIYDKNLLMIKEHILA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                             691 QKGNNYKMYSEFKSIKPEVYLKKYSEKCSNLNFEDEFKEELHSDYKNK-CT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 KIADHDVTTAKKKITAVFQKIGSKTTNGKKV------LEREGWWKEYGLSIWKGMLCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 EAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                       92660
                                                                                 SSEE: Knobbe Martens Olson & T: 620 Newport Center Drive Newport Beach California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IETLKVEC -
                                                                                                                                                                                                                                                                                                                                                             Application US/08568459A
                                                                                                                                                                                                                                     Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
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                                                                                                                                                                                      AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                      Thomas E.
BINDING DOMAINS FROM PLASMODIUM VIVAX
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24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KEKPCEDDN----CKSKCNSYKÉWISKKKEEYNKQAKQYQEY
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16th
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Search completed: June 20, 2003, 15:07:02 Job time : 20.1745 secs
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DO SOFTWARE: PatentIn Relaction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                           255 OCKOYHSWIGIW 266
                                                                                        275 OCEKYKKWMERW 286
                                                                                                                         200 XXXXRPQFLRWLTEWGENFCKEQKKEYKVLLAK---CXXXXXXXXXXXXC--XXXCVACKD
                                                                                                                                                    215 EFASRPPFLRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKT 274
                                                                                                                                                                                     161 LEREGWWKEYGLSIWKGMLCAL-----SYNTETKKMDEGVRTYLMKYIYKNNDIKEYLE
                                                                                                                                                                                                                                                                         101 DMIPPEFFRSMFYTFGDYRDICLDTDISEKIADHDYTTAKKKITAVFQKIGSKTTNGKKV 160
                                                                                                                                                                                                                                                                                                                              43 CMPPRRQNLCVHYL--TKLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHR 100
                                                                                                                                                                                                                                                85 XXXXXDFKRQMFYTFADYRDICLGTDISSK----KDTSXXXXXXXXXXXXXXXXKISN--SI 139
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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PatentIn Release #1.0, Version #1.25
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Pred. No. 5.3e-18;
5; Mismatches 145
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Database :
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Listing first 45 summaries
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Gapop 10.0 ,
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1913
                                             417779 seqs, 108206813 residues
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/cgn2_6/ptodata/2/pubpaa/US08_
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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US-10-153-273-17
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                                                                                                                                                                                                        Sequence 8, Appli
Sequence 12, Appli
Sequence 6, Appli
Sequence 15, Appl
Sequence 14, Appl
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Sequence 17, Appl
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Sequence 20, Appli
Sequence 10, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence
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89.5	89.5	90	90	91	93	93	94.5	94.5	95	95	95	97	97	97	97	97.5	98	98	98	98.5	99	101	101	101	101
4.7	4.7	4.7	4.7	4.8	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.3	5.3	5.3	5. 3
670	621	610	610	315	654	380	2353	271	1475	716	677	711	411	208	208	665	1805	456	380	1092	874	1979	1972	1945	1938
9	10	9	9	9	10	10	10	9	10	10	10	9	9	10	9	ဖ	9	10	10	9	9	9	9	9	9
US-09-298-523B-63	US-09-856-247A-2	US-10-205-823-357	US-09-802-640-36	US-10-106-698-5557	US-09-952-013A-5	US-09-134-333-12	US-09-797-862-33	US-10-153-273-14	US-09-740-274-2	US-09-815-242-12403	US-09-745-763-168	US-09-298-523B-3	US-10-153-273-19	US-09-925-637-52	US-10-084-205-52	US-09-820-843A-107	US-09-820-843A-73	US-09-925-300-1595	US-09-134-333-13	US-09-423-126-5	US-09-893-519A-50	US-09-927-597-4	US-10-171-311-162	US-09-927-597-2	US-10-171-311-164
Sequence 63, Appl	Sequence 2, Appli	Sequence 357, App	Sequence 36, Appl	Sequence 5557, Ap	Sequence 5, Appli	Sequence 12, Appl	Sequence 33, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 12403, A	Sequence 168, App	Sequence 3, Appli	Sequence 19, Appl .	Sequence 52, Appl	Sequence 52, Appl		Sequence 73, Appl	Sequence 1595, Ap	Sequence 13, Appl	Sequence 5, Appli	Sequence 50, Appl	Sequence 4, Appli	Sequence 162, App	Sequence 2, Appli	Sequence 164, App

## ALIGNMENTS

RESULT 1 US-10-153-273-8

Sequence 8, Application US/10153273 Patent No. US20020169305A1 GENERAL INFORMATION:

APPLICANT:

Sim, Kim L.

Chitnis, Cherry Miller, Louis H.

Su, Xin-zhaun

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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      REFERENCE/DOCKET NUMBER: NIH121.1FWDV1 TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                          TELEPHONE: (61 TELEFAX: (619)
                                                                                                                                                                                                  APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wellems, Thomas E.
INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                       ID NO:
                                                                 (619)
                                            235-0176
                                                                                                                                   36,516
                                                                                                                                                                                                                                                                                                                                                           Version #1
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TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium fa

SEQUENCE DESCRIPTION: SEQ ID
US-10-153-273-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-10-13-273-12
Sequence 12, Application US/10153273
Patent No. US20020163305A1
GENERAL INFORMATION:
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Local Similarity 41.0%;
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      NUMBER OF SERVE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
ADDRESSEE: Knobbe Martens Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625 LTEWGENFCKEQKKEYKVLLAKCKDCDVDGDG----KC--NGKCVACKDQCKQYHSWIGI 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT 114
      ¿APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CKMYQKLISEQIEKNNIHNCKKTED-AKWKCENT--KLGEDEGVCMPPRRQNLCVHYLIK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMER 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WIDNYKKQKGRYTEVK-
                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKKHYSSOKKKFOLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTOLEN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWKGMLCALSYNT-----ET-KKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FADYRDICLGTDISSKKDTSKGVGKVKCNIDDVFYKISN-----SIRYRKSWWETNGPV 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGDYRDICLDTDI-SEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMTNTNE--LKYAFIKCAAAETFILWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IWEGMLCALSYDTSLNNVNPETHKKLTEGNNNF-EKVIF-GSDSSTTLSKFSERPOFLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 921 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                                                  Peterson, David S. Su, Xin-zhaun Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      m, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                     Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 646; DB 9; Pred. No. 5.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   falciparum ID NO: 8:
                                                                                                                                                                                                                                                                                                                                     FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                  Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 921;
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                                                                                                                                                                                                                                                              RESULT 3
US-10-153-273-6

Sequence 6, Application US/10153273
Patent No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sin, Kim L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium falciparum SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-153-273-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 137; Conserv
                                                                                              NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS:
                                                                                                                                                  Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1584
                                                                                                                                                                                                                                                                                                                                                                                                                                               1636 FYLKANVQPQD-----PEYKGYEYKDGVQPIQGN-----EYLLQKCDNNKCS 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1469 YRDICLNTDISKK--QNDVAKAKDKIGKFFSKDGSKSPSG---LSRQEWWKTNGPEIWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1524 MLCALTKYYTDTDNKRKIKNDYSYDKVNQSQNGNPSLEEFAAKPQFLRWMIEWGEEFCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1409 QTENIKTDDNLKDAFIKTAAAETFLSWQYYKSKNDSEAKILDRGLIPSQFLRSMMYTFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1349 CKIVEKILEGKNGRTTVGECNPKESYPDWDCKNNIDISHDGACMPPRRQKLCLYYIAHES 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YRDICLDTDISEKIADHDVTTAKKKITAVFOKIGSKTTNGKKVLEREGWWKEYGLSIWKG 177
        STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQLENMICT
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COUNTRY: US
                                                                         ADDRESSEE: Knobbe Martens Olson &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA
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Miller, Louis
                                                                                                                                                                                                                            Peterson,
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                                                                                                                                       AND PLASMODIUM
                                                                                                                                                                                                                       Louis H.
, David S.
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                                                        Bear
16th Floor
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                                                                                                                                     ERYTHROCYTE
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                                                                                                                                     BINDING PROTEINS
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ZIP: 92660 COUNTRY: US 679

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Matches Query Match

Conservative

CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE: Floppy disk

: 92660 READABLE FORM:

SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER

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US-09-924-154-15
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                                                                                                       RESULT 4
            Sequence 15, Application US/09924154
Patent No. US20020127241A1
GENERAL INFORMATION:
APPLICANT: Narum, David L.
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 235-0
TELEPHAX: (619) 235-0
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Plasmodium SEQUENCE DESCRIPTION: SEQ
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                                                                                                                                                                                                                                                                                                                                242 VSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 DISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVL---
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                                                                                                                                                          MVCEN 397
                                                                                                                                                                                                                                                                                                   KOLEKICE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQIEKNNIHNCK---KTEDAKWKC-ENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002 CLASSIFICATION: <Unknown>
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Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                     -VKHIPKGKTCKRH-NNFEKIPQFLRWLKEWGDEFCEEMGTEV
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                                                                                                                                                                                                                                                                                                 NKNCSEKK----CKNACSSYEKWIKERKNEYNLQSKKFDSDK
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Pred. No. 6.8e-21;
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9 ISEQIEKNNIH----NCKKTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDSK 64

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RESULT 5
US-09-924-154-14
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                                                                                  US-09-924-154-14
         Matches
                                                                                                                                     SEQ ID NO 14
LENGTH: 1143
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09924154 Patent No. US20020127241A1
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Best Local Similarity
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                                          Query Match
                          Best Local
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                       APPLICANT: Narum, David L. APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                        SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105
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TYPE: PRT
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                                                                                                   ORGANISM: Mammalian
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       Conservative
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                                                                                                                                                                      version 3.1
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28.2%;
                          17.4%;
27.9%;
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Score 333.5; DB 10,
Pred. No. 4.8e-19;
Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 353; DB 10;
Pred. No. 1.1e-20;
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RESULT 6
US-10-153-273-4
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                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    ORIGINAL
                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                     HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKMYDNIDEVKNKEANVYLKEKSKECKDVN 724
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                                                                              STRANDEDNESS: single
                                                                                                        TYPE: amino acid
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                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 620 Newport Center Drive CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe Martens Olson & Bear
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                                                                                                                             LENGTH:
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
  SOURCE:
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Wellems,
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Miller, Louis H.
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105 CURRENT APPLICATION NUMBER: US/09/924,154 CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Narum, David APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                     182 LSYNTETKKMDEGVRTYLMKYIYKNNDI-KEYLEEFASRPPFLRWYTEWGEDFVKNRKKE
                                                                                562 DLSNRKL
                                                                                                                                                                 519 IAIYES----RILKRKYKNKDDKEVCKIINK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 DKNSV----DTNTKVWECKNPYILSTKDVCVPPRRQELCLGNIDRIYDKNLLMIKEHILA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 KNSATYNNGLAVKEANSETY--KNDPEVTEANSAKHARDYLKTQLENMICT 349
                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                      14 EKNNIHNCKKTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDS----KEEDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 EAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 EKNNIHNCKKTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDS----KEEDLR 69
                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                      KIADHDVTTAKKKITAVFQKIGSKTTNGKKV----
                                                                                                                                                                                                     EAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKGNNYKMYSEFKSIKPEVYLKKYSEKCSNLNFEDEFKEELHSDYKNK-CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSYNTETKKMDEGVRTYLMKYIYKNNDI-KEYLEEFASRPPFLRWVTEWGEDFVKNRKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIADHDVTTAKKKITAVFQKIGSKTTNGKKV-----LEREGWWKEYGLSIWKGMLCA 181
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.2%;
24.8%;
                                                                                                                                                                                                                                                                                                                                                 16.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KEKPCEDDN----CKSKCNSYKEWISKKKEEYNKQAKQYQEY
-VISWVFKDKTVCKE--DDIENIPQFFRWFSEWGDDYCQDKTKM
                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                          Score 312; DB 10;
Pred. No. 3.8e-17;
1; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 329; DB 9; Pred. No. 1.5e-18;
                                                                                -VGKINTNSNYVHRNKQNDKLFRDEWWKVIKKDVWN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VGKINTNSKYVHRNKKNDKLFRDEWWKVIKKDVWN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 113;
                                                                                                                                                                                                                                                                                                                            117;
                                                                                                                  -LEREGWWKEYGLSIWKGMLCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1435;
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                                                                                                                                                             ----TFADIRDIIGGTDYWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 88;
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Gaps

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RESULT 8
US-10-153-273-17
; Sequence 17, Application US/10153273
; Patent No. US20020169305A1
; GENERAL INFORMATION:
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                                                                                                                             Matches
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL INFORMATION.

APPLICANT: Sin, Kim L.

Chitnis, Chetan

Miller, Louis H.

Posterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May.2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE MATTERS Olson & Bear
ADDRESSEE: Knobbe Martens Olson & Bear
ADDRESSEE: Knobbe Martens Olson & Bear
ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691 QKGNNYKMYSEFKSIKPEVYLKKYSEKCSNLNFEDEFKEELHSDYKNK-CT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKFQLY 300
101 DMIPPEFFRSMFYTFGDYRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKV 160
                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IETLKVEC-----KEKPCEDDN----CKRKCNSYKEWISKKKEEYNKQAKQYQEY 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fuller, Michael REGISTRATION NUMBER: 36,516 REFERENCE/DOCKET NUMBER: NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNSATYNNGLAVKEANSETY--KNDPEVTEANSAKHARDYLKTQLENMICT 349
                                       CMPPRRQNLCVHYL--TKLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMMUNICALL...
TELEPHONE: (619) 235-000
7619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wellems, Thomas E.
INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92660
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                                                                                                                                               14.8%; Score 284; DB 9; 29.4%; Pred. No. 1.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <Unknown>
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                              Length 324;
                                                                                                                           Indels
                                                                                                                           18;
                                                                                                                         Gaps
                                           84
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                                                                              SEQUENCE
US-10-153-273-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21,
Query Match
Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEVEL...
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson &
ADDRESSEE: Anobbe Martens Olson &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIEICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                         ORIGINAL
                                                                                                                                             FRAGMENT TYPE: internal
                                                                                                                                                                HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BINDING
                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 QCEKYKKWMERW 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 XXXXRPQFLRWLTEWGENFCKEQKKEYKVLLAK---CXXXXXXXXXXXXC--XXXCVACKD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 EFASRPPFLRWYTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 RYRKSWWETNGPVIWEGMLCALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 LEREGWWKEYGLSIWKGMLCAL-----SYNTETKKMDEGVRTYLMKYIYKNNDIKEYLE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 XXXXXDFKRQMFYTFADYRDICLGTDISSK---KDTSXXXXXXXXXXXXXXXXXXXXXISN--SI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCKQYHSWIGIW 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fuller, Michael REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619)
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619)
                                                                                                                                                                                                                                                                                            LENGTH: 311 amino acids
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  Conservative
                                                                                                      DESCRIPTION: SEQ
                                                                                                                           SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20169305A1
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Peterson, David S.
Su, Xin-zhaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sim, Kim L.
Chitnis, Chetan
                   14.2%;
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                                                                                                                                                                                                                                                                                                                                                           235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas E.
  22;
Score 272.5; DB Pred. No. 1e-14; Pred. No. 1e-14; Pred. Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         36,516
                                                                                                      ij
                                                                                                      NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     NIH121.1FWDV1
                                                                                                        21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version
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16th Floor
                                       DB 9;
  140;
                                       Length 311;
  Indels
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Gaps

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Sequence 2, Application US/10153273 Patent No. US20020169305A1 GENERAL INFORMATION:
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3-10-153-273-2
                                                                                                                                                                           TELEFAX: (619) 235-0:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    SEQUENCE
                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKKWMERWKK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPQFLRWMIEWGEEFCAERQKKENIIKDACXX-----XXXXXXXCXXXKH--RCNQACRA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPFLRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLEREGWWKEYGLSIWKGMLCAL-SYNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFAS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDMIPPEFFRSMFYTFGDYRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMPPRRQNLCVHYL---TKLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILH
ORGANISM: Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                          LENGTH: 1115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wellems, Thomas E.
INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson, Dav
Su, Xin-zhaun
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Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                    235-0176
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US-10-153-273-10
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Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application Patent No. US200201693 GENERAL INFORMATION:
                    INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPUTER
                                                                          NAME: Fuller, Michael REGISTRATION NUMBER: 36,516 REFERENCE/DOCKET NUMBER: NIH121.1FWDV1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
  SEQUENCE
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KKTISSAIINHAFLQNTVMKNCNYKRKRRERDWDC-NTK----KDVCIPDRRYQLCMKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US20020169305A1
                                   TELEFAX: (619) 235-85
TELEFAX: (619) 235-0176
                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: CUnknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKL--NDDS----KEEDLREAFIK-----SAAAETFLLRQYYNSKNVEDDKILHRDMIPPE
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                                                                                                                                                                           APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & STREET: 620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wellems, Thomas E
OF INVENTION: BINDING
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Su, Xin-zhaun
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                    ID NO:
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26.2%; Pred. No. 1e-13;
Live 50; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas E
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16th Floor
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487 282

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ORGANISM: Plasmodium falciparum ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-10-153-273-10
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                                                                                                                                             ; ORGANISM: Mammalian US-09-924-154-16
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09924154 Patent No. US20020127241A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 16
                                                                                     Query Match
Best Local S
                                                                          Matches
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use FILE REFERENCE: 05213-0465 43170-262105 CURRENT APPLICATION NUMBER: US/09/924,154 CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Narum, David APPLICANT: Sim, Kim L.
                                                                                                                                                                           LENGTH: 97
TYPE: PRT
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                                                                        70;
                                                                                       Similarity
                    CK-KTEDAKWKCENTKLGEDEGYCMPPRRQNLCVHYLTK---LNDDSKEEDLREAFIKSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHYSSQKKKFQ----------LYKNSATYNNGLAVKEANSETYKNDPEVTEA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKQC-----RDYEQNLYCSGNGYDCTKTIYKKGKLVIGEHCTNCSVWCRMYETWIDNQK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYFIKTACNVGKGTNGQCHCIGGDVPTY----FDYVPQYLRWFEEWAEDFCRKKKKKLENL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYLMKYIYK------NNDIKEYLEEFASRPPFLRWVTEWGEDFVKNRKKELVSL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKDVMKTNGAQERYIDDAKGGDFFQLREDWWTSNRETVWKALICHAPKEA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSKT--TNG--KKVLE------REGWWKEYGLSIWKGMLCALSYNTETKKMDEGVR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCTVLARS-----FADIGDIVRGKDLYLGYDNKEK---EQRKKLEQKLKDIFKKI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KILHRDMIPPEFFRSMFYTFGDY---RDICLDTDISEKIADHDVTTAKKKITAVFQKI 150
CKEKGNDKIWQCINEHIKDFPDVCGPPRRQQLCLGNLDKDEFKNVNDLKKFLNEIILGIR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEFLKOKRKYETEISGGGSGKSPKRTKRAARSSSSSDDNGY----ESKFYKKLKEVGYQ 330
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                            David L.
                                                                                    11.8%;
23.3%;
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Pred. No. 7.7e-11;
                                                                                       Score 226.5; DB 1
Pred. No. 2.8e-10;
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                                                                      Mismatches
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                                                                                                      DB 10;
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                                                                                                      Length 972;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Narum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and FILE REFERENCE: 05213-0465 43170-262105
CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
RESULT 14
US-10-153-273-15
; Sequence 15 Application US/10153273
; Patent No. US20020169305A1
; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09924154 Patent No. US20020127241A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                          128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                       277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 N 308
                                                                                                                                                                               243 -SLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 VQRSYIRGCKGKRSTHTWICENK---GNNNICIPDRRVQLCITALQDLKNSGSETTDRKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 IEKNNIHNCK-KTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYLTKL-NDDSKEED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                            TKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGE---DFVKNRKKELV-- 242
                                                                                                                                                                                                                                                                                                                                    SEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCALSYNTE 187
                                                                                                                                                                                                                                                                                                                                                                                                                     LREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIDKKVKSPKPSENPSD----VATVCNKSCTDYDKWIINKRKEYKMQSSKYK--RDRSLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKFQLYKNSATYN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEKTADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCALSYNTE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAETFLLRQYYNSKNVEDDKILHRDM-IPPEFFRSMFYTFGDYRDICLDTDI------
                                                                                                                                                                                                                     CRKPDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWVTEWGEDFVKNRKKELVSLKKK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TENILKGNFEGIKANIVSMYPSYADLSLDE----FRKHWWDQNKKQLWEAISCE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGKFLIEKY-----RKNMHENMYLDERACKYLNYSFDDYKNIILGKDMWRDPNSIK 249
                                                                                                                                                                                                                                                                                                 DKNNISKLVEESLKRF---FKKDSS------VLNPTAWWRRYGTRLWKTMIQPYAH-LG
                                                                                                                                                                                                                                                                                                                                                                                LRDKVFDSAMYETDLLWNKYGFRGFDD------FCDDVKNSYLDYKDVIFGTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- FYKGNHTGVCLMEDDNDNQYLHWFREWKNDFCIDKLKWNDVIKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 220; DB 10;
Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                          -GCNNECYTYRSLINRQRYEVSILGKKY 351
                                                                                                                                                                                                                       NEPQINRWILEWGKYNCRLMKEKEKLLTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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APPLICANT:

sim,

Kim L.

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est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 235-0 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                               164 FFRWFSEWGDDYCQDKTKMIETLKVEC
                                      281 KWMERWKK 288
                                                                                                                   222 FLRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTC-DDNENCGACKTQCEKYK 280
                                                                                                                                                                                                     162 EREGWWKEYGLSIWKGMLCALSYNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPP 221
                                                                                                                                                                                                                                                                                    102 MIPPEFFRSMFYTFGDYRDICLDTDISEKIADHDYTTAKKKITAVFQKIGSKTTNGKKVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                             42 VCMPPRRQNLCVHYLTKLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/210,288 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
  EWISKKKK 216
                                                                                                                                                              FRDEWWKVIKKDVWN----VISWFXXXXXCXXXXXXXI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fuller, Michael REGISTRATION NUMBER: 36,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson, David S. Su, Xin-zhaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitnis, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acids
                                                                                                                                                                                                                                             -TFADIRDIIGGTDYW-----NDLSNRXXXXXXXXXXXXXXXXXKKNDKL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 171; DB 9;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                 -CKSKCNSYK 208
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                              -PQ 163
                                                                                                                                                                                                                                                                                                                                 84
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RESULT 15
US-10-153-273-20
; Sequence 20, Application U
; Patent No. US20020169305A1
; GENERAL INFORMATION:
                                                                                                               QΥ
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                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
  284
                                       281
                                                                            227
                                                                                                               223 LRWYTEWGEDFYKNRKKELVSLKKKCDSCTLRNNGTSNKTC-DDNENCGACKTQCEKYK- 280
                                                                                                                                                          190 RADWWEANRHQVWRAMKCATXXXX--
                                                                                                                                                                                             163 REGWWKEYGLSIWKGMLCALSYNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPF 222
                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/153,273 FILING DATE: 21-May-2002
EIEKWNEQWRK
                                       ---KWMERWKK 288
                                                                        LRWMTEWAEWYCKAQSQEYDKLKK---ICXXXXXXXXXXXXXXXXXXXXCKCKAACDKYKE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10153273
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                            SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IION:
: Sim, Kim L.
: hands, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Su, Xin-zhaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (619) 235-8550
  294
                                                                                                                                                                                                                                                         26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235-0176
                                                                                                                                                                                                                                    Score 144.5; DB 9;
Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                                       20:
                                                                                                                                                                                                                                                                           Length 411;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                            ----CXXXXXXXXIPQR 226
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Search completed: June 20, Job time: 38.7511 secs

2003,

15:18:24

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, sing sw model

Run on: June 20, 2003, 14:59:06; Search time 27.6965 Seconds (without alignments) 1218.319 Million cell updates/sec

US-10-087-013-9 1913

Title: Perfect score:

Sequence: 1 PCKMVQKLISEQIEKNNIHN.....AKHARDYLKTQLENMICTNG 351

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

arched: .

283224 seqs, 96134422 residues

l number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13				9		7	O	υı	4					Result
115	115.5	116.5	116.5	117.5	٠	118	122.5	127.5	171.5	254	261	269	329	360.5	374.5	375	397.5	398.5	399.5	403.5	432	433.5	443	501	520	547.5	562.5	625.5		SCOTE
6.0	6.0	6.1	6.1	6.1	6.1	6.2		6.7			13.6	14.1	17.2		9	9	0	0	0	21.1	2	2	ω	σ.	7	8	29.4	32.7		Query
944	2401	346	335	1004	911	3844	690	1123	778	1045	1153	1070	1435	1729	2182	2228	2135	2197	2664	2647	2924	2042	2212	3006	2706	1711	3026	3078		I pnath
2	2	N	N	N	2	N	N	N	N	N	N	N	N	N	N	2	Ν	N	N	N	ນ	N	2	2	N	N	N	2	, 6	D
S26710	28	F87844	T25110	JC2221	S51441	T18402	151298	T28139	A35970	T18373	T28652	T30848	A37793	T18396	T28634	T14029	T14602	B71600	T28626	T28161	T18378	T18399	T28157	T28625	T28155	C71625	T28431	T28432		7
													•																	
	protein -			т	hypothetical prote	asparagine/asparta	transforming prote	PK4 protein kinase	erythrocyte-bindin		ndi	Duffy receptor - P	erythrocyte-bindin	ĸ	variant-specific s		variant-specific s		ific	ct	variant-specific s	variant-specific s	erythrocyte membra	variant-specific s	variant-specific s	-specific	surfac	variant-specific s		7

RESULT 2 T28431 variant surface protein 1 homolog A4VAR - malaria parasite (Plasmodium falciparum) (f

45	44	43	42.	41	40	39	3 8	37	36	ა 5	34	ω ω	32	31	30
107	107.5	108	108	109	109	109	110	110.5	110.5	111.5	111.5	113	114	114	114
5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.8	5.8	5.8	5.8	5.8	5.9	6.0	6.0	6.0
657	2910	3335	508	2139	845	482	1995	1712	1346	1939	837	1390	2269	993	981
N	N	N	2	N	N	N	N	N	ผ	N	N	N	N	N	2
G71602	T28156	H81702	E71620	T18296	148176	T24518	T08166	C71618	G71613	T18372	T48407	S51364	T28677	S49461	C82930
protein with DnaJ	DNA-directed RNA p	adherence factor T	hypothetical prote	myosin heavy chain	synaptonemal compl	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	repeat organellar	hypothetical prote	sperm tail-specifi	rhoptry protein -	synaptonemal compl	pll5 protein UUl40

## ALIGNMENTS

Qy	Qy Db	Qy Db	Qy Db	Qy Db	Que Ma	T28432 Varian N;Alte C;Spec C;Date C;Date C;Date C;Su, Cell A;Titl A;Titl A;Stace A;Acce A;Acce A;Acce A;Acce A;Gene A;Intr
237 RKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMÉRWKKHYSSQKKK 296	178 MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKBYLEEFASRPDFLRWYTEWGEDFVKN 236 	118 YRDICLDIDISEKIADHDVITAKKKITAVFQKIGSKTINGKKVLEREGWWKEYGLSIWKG 177       :   :   :	58 KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD 117 : :::::::: ::   :                :	. 2 CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENTKLGEDEGVCMPPRRQNLCVHYLT 57   : : :	Query Match 32.7%; Score 625.5; DB 2; Length 3078; Best Local Similarity 38.8%; Pred. No. 4.7e-35; Matches 137; Conservative 61; Mismatches 126; Indels 29; Gaps 9;	RESULT 1 T28432 N;Alternate names: erythrocyte membrane binding protein 1 (EMPI) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Ancession: T28432 A;Reference number: 220487; MUID:95330813; PMID:7606788 A;Residues: Preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-3078 <sux> A;Residues: 1-3078 <sux> A;Cross-references: EMBL:L40608; NID:9886374; PID:9886375; PIDN:AAA75396.1 C;Genetics: A;Gene: var-1 A;Introns: 2611/3</sux></sux>
-	23 <i>7</i> 1582	178 MLCALS-YNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRPPFLRWYTEWGEDFVKN	118 YRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKG       :    :     :	58 KLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGD : ::: ::   :	2 CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENTKLGEDEGVCMPPRRONLCVHYLT     :   :	Query Match  32.7%; Score 625.5; DB 2; Length 3078;  Best Local Similarity 38.8%; Pred. No. 4.7e-35;  Best Local Similarity 38.8%; Pred. No. 4.7e-36;  Best Local Similarity 38.8%; Pred

1081

1021

969

248

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A:Molecule type: DNA
A;Residues: 1-1711 <GAP>
A;Cross-references: GB:AE(
A;Experimental source: clC:Genetics:
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium A;Reference number: A71600; MUID:99021743; PMID:9804551
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C; Date: 15-Oct-1999
C; Accession: T28431
R; Smith, J.D.; Kyes,
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A;Title: Analysis of adhesive domains from the A4VAR Plasmodium A;Reference number: Z20486; MUID:99094502; PMID:9879893
A;Accession: T28431
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A; Residues: 1-3026 <
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                              Query Match
Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                              Status: preliminary; nucleic
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                          Score 547.5; DB 2;
Pred. No. 6.2e-30;
3; Mismatches 105;
                                                                                                                                                       GB:AE001362; NID:g3845070; PIDN:AAC71792.1; PID:g38450
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Pred. No. 1.1e-30;
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N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28155
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A;Title: Plasmodium falciparum rosetting is mediated A;Reference number: Z20477; MUID:97373957; PMID:92304
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A; Residues: 1-2706 <
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YMRKKKEEWNLQDKYYKDKRENKGIDKGPIGIIVKDYVLANAKEYLKKKFTASCVTSSGK 1096
                                                                                                         FLRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKK
                                                                                                                                                                                                                                                      YRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKG
                                                                      FLRWFVEWYDDYCKERQKYLTEVASTCKSI----DGGQLK-CD-----RGCNNKCDEYKK
                                                                                                                                                                                   MLCALSYNTETKKMDEGVRTYLMKYIYKNNDIKEY---
                                                                                                                                                                                                                                                                                                                  LNDDSKEEDLREAFIKSAAAETFLL-RQYYNSKNVEDDKTLHRDMIPPEFFRSMFYTFGD
                                  WMERWKKHYSSQKKKFQLYKNSATYNN---GLAVKE---ANSETYKNDPE----VTEANS 331
                                                                                                                                                                                                                      FRDFCLENDMGK-----DVDKVKKNINKVF---NNSSKRGFKKIDPENWWNENGPQIWNG
                                                                                                                                                                                                                                                                                           EEQTKNKYQLREAFIKCAAKETNLLWDKYKNDKN-EAEELLKKGKIPEDFMRIMFYTFGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <ROW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAA73831.1
4/25/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 520; DB 2;
Pred. No. 8.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
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                                                                                                                                               - IKNKDNYKYEKVTILAKRDGSNGMTLSEFAKKPK
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140
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complemen

281 1036

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221

939 177 117 828

17;

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erythrocyte membrane protein 1 - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-20(C;Accession: T28157 R;Yang, S.Q.; Wollish, W.S.; Gut, J.; Wu, J.; Ahn, J.; Petersen, C.; Fujic submitted to the EMBL Data Library, July 1995 A;Bescription: The molecular cloning and DNA sequence analysis of Plasmod: A;Beference number: Z20479 A;Accession: T28157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variant-specific surface protein 3 - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T28625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The large diverse gene family var encodes proteins involved in cytoadherence A;Reference number: 220487; MUID:95330813; PMID:7606788
A;Accession: T28625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 82, 89-100, 1995
A;Molecule type: DNA
A;Residues: 1-2212 <YAN>
A;Cross-references: EMBL:U31083; NID:g1517813; PID:g1517814; PIDN:AAB06961.1
                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 2597/3
                                                           A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              olecule type: DNA sidues: 1-3006 <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oss-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1933
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                                                                                                                                                                                                                                                                                                                                                                                                             2053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1813 KIEGVDTTVSSDGETTTPITHDALREAFIQTAAVETFFLWHRYKKIKEKERQEELQNGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1993 HNTDTRQVDDQVKGQLFENGKNTPKNSQYQYKNVTISSVSSNGGPIGNIKLEQFASRPTF 2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 YL----TKLNDDSK------EEDLREAFIKSAAAETFLL-RQYYNSKNVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PCKMVQKL-----ISEQIEKNNIHNCKKTEDAKWKCENTKLGEDEGVCMPPRRQNLCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                   TLKCPSCAKSCKSYKKWISRKKDEFTKQKGAYEKQKKDAEGNNN-DYKEF-SKTLRN 2160
                                                                                                                                                                                                                                                                                                                                                               --NCGACKTQCEKYKKWMERWKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKN 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNE--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNTETKKMDEGVRTYLM-----KYIYKNNDIKEY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNKSGDKNIKDISEKIKSVIEKSGEQTPPGPKPGQTTTKPEEWWQKNGEHIWNAMICALT 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCDIVKTLFTTTETLKEACPTKYVNGREKFPN--WKCISSGSDASGSICIPPRRRKLYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQNSATEEVKKNIE 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKH-ARDYLKTQLE 344
                                                                                                                                                                                                                                                                                                                                                                                                             LRWLEEWGEEFCRKQYHKLERIKEEC------HKDGNRNCDDDGFECKEMCPCKDGSFE 2105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL:L40609; NID:g886376; PID:g886377; PIDN:AAA75397.1
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Pred. No. 2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from GB/EMBL/DDBJ
                                                             from GB/EMBL/DDBJ
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                                                                                                                                                         Petersen, C.; Fujioka,
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                                                                                                                                                                                               09-Jun-2000
                                                                                                                       Plasmodium
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                                                                                                                                                                                                                   A; Note:
                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                           A;Cross-references:
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-2042 < RUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sin
Matches 128;
                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                           Query Match
Best Local :
                                                                                                                                         Matches
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                                                                                                                                         Conservative
     22.7%;
25.1%;
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R;Rubio, J.P.; Thompson, J.K.; Cowman, A.F.

BMBO J. 15, 4069-4077, 1996
A;Title: The var genes of plasmodium falciparum are located
A;Reference number: Z18927; MUID:96324414; PMID:8670911
A;Accession: T18399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: EMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant-specific surface protein 1 homolog 3D7var1 - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18399
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 GSPVTSNSGSICIPPRRRRL---YIQKLHDWASGNTVVSGQAQTPQGGTSSPSGKETPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1272 IVAGVLTKENLENACPTKYGPKAPTSWKCIPTEKTNAATGSEGSSGNGALQRAKRATVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1626 KRLEKIKVEC----MDEDGKKQKCSGDGEDCEEIRKQDYSTVRDFYCPECGKYCRFYKRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 DLREAFIKSAAAETFLL-RQYYNSKNVE-----
                       38 - EDEGYCMPPRRQNLCVHYLTKLNDDSKEEDLREAFIKSAAAETFLLRQYYNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LISEQIEKNNIHNCKKTE-----DAKWKC-----ENTKLGED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERWKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKKPKDQKYQYDKVKLDENSGTSPKTNDHVPPTPLTNFISRPPYFRYLEEWGETFCRERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----MKYIY------KNND--IKEYLEEFASRPPFLRWVTEWGEDFVKNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADSQPPSDEK---RQTWWEQNGEHIWNGMICALTYKEKDEKGTPLKQNEGLKSALWDEK 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GSKTTNGKKVLEREGWWKEYGLSIWKGMLCALSYNTETK----KMDEGVRTYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILHRDMIPPEFFRSMFYTFGDYRDICL---DTDISEKIADHDYTTAKKKITAVFQKI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLRTAFIQSAAIETFFLWDRYKKEKEIEKKEKKVANGGLVPSLNGGPPQQPGVTGDSPQS
                                                                                                                         PCKMVQKLISEQIEKNNIHNCKKTEDAKWKC-----ENTKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEKKKDEYDKQKEAYNNQKTDARRNN---
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                                                                        PCKIVEELFKSTKNFEDACGLKYGKNYGWKCVHHTSDKGSEPTARGHSHVARSADGAPSG
                                                                                                                                                                                                                                                                                                                                                   EMBL: U53324; NID: g1297090; PID: g1297091;
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Pred. No. 1.5e-22;
9; Mismatches 133;
                                                                                                                                                                                               Score 433.5; DB 2;
Pred. No. 6.1e-22;
                                                                                                                                                                          Mismatches, 142;
:: =: =: = = =
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                                                                                                                                                                          Indels
                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                   PIDN: AAB09769.1
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A;Title: Cloning the P. falciparum gene encoding pfEMP1, A;Reference number: 218925; MUID:95330812; PMID:7541722
A;Accession: T18378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 15-Oct-1999
C; Accession: T18378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant-specific surface protein 1 - malaria parasite (Plasmodium N;Alternate names: erythrocyte membrane binding protein 1 (EMP1) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 09
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                                                                                                                                                          DSKEEDLREAFIKSAAAETFL----LRQYYNSKN---
                                                                                                                                                                                           VPPRRRKL---YVGKLHDWAGGETTEAKSQETSGGQKTPSGNESSPSEKLPQGPTPETTK 955
                                                                                                                                                                                                                                                               CSIVDKALKGKLDDACTLKYGKTAPTSWKCIPSGNNTTTESTTKPGAAGTPSGKDTGSIC
                                                       KTGHIPPDFLRQMFYTLGDYRDILVGNTDIVVHTSGNKEDMQIMEAIQKKIEQILPTSGS
                                                                           HRDMIPPEFFRSMFYTFGDYRDICL-DTDI----SEKIADHDVTTA-KKKITAVFQKIGS
                                                                                                                      ETPESSLLHAFVSPFRLRRFLPWHKFKEQWKAQHGAGATGQQTIIGTLDGGGEETPDKLL 1015
                                                                                                                                                                                                                                                                                                   CKMVQKLISEQIEKNNIHNCKKTEDAKWKC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSDIVSGDNVIKERENTIKEKIASFFQNGNKEGTPHVPKNPVQTPQTWWKDNAKHIWHGM
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                                                                                                                                                                                                                                                                                                                                         Conservative
     EMBL:U27338; NID:g914918; PID:g914919;
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                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                    Score 432; DB 2;
Pred. No. 1.2e-21;
9; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note:
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A; Residues: 1-2647 <HER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Expressed var genes are found in plasmodium A; Reference number: 220483; MUID:97154495; PMID:90012
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R; Hernandez-Rivas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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les 125; Conserva
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            CKTQCEKYKKWMERWKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKNDPEVTEANS
                                             EWAETFCRERKKRLEKIKVEC----MDEDGKKOKCSGDGEDCEEIRKODYSTVRDFYCPE 1678
                                                                                 EWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNEN
                                                                                                                                                                                                                                                      NYNKTCVIPPPFLRQMFYTLGDYADIFFGKNDIVIDTKNGDKDIAEREKKIKDAIERVLK
                                                                                                                                                                                                                                                                                                                                                DLREAFIKSAAAETFLLRQYY------
                                                                                                                 NKKPKDQKYQYD----KVKLDENSGTSPKIVVPAPKPTTTEPPPPSPTSFSRPPYFRYLE 162:
                                                                                                                                                                                     NADSQPPSDEK----RQTWWEQNGEHIWNGMICALTYKEKDEKGTPLKQNEGLKSALWDEK 1566
                                                                                                                                                                                                                                                                            ----EGVCMPPRRQNLCVHYLTKLND---
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                                                                                                                                                     -----MKYIYKNNDIKEYLEEFA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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be: strain FCQ27/PNG
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Pred. No. 1e-19;
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PMID:9001213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.; Peterson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                      -KMDEGVRTYL----
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                                                                                                                                                   SRPPFLRWVT
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RESULT 11
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wariant-specific surface protein 1 homolog PFB1055c - ma
variant-specific surface protein 1 homolog PFB1055c - ma
N;Alternate names; erythrocyte membrane binding protein
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Su, X.Z.; Heatwole, V.M.; Wertheimer, Cell 82, 89-100, 1995
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Note: var-2
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sidues: 1-2664 <SUX>
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13-Nov-1998 *sequence_revision 13-Nov-1998 *text_change 21-Jul-2000
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24; Conservative
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                                                                                                                                                                                                                                                                                       DSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKFQLYKNSATY--
                                                                                                                                                                                                                                                                                                                           AKTPSASSDTPLLSDFVLRPPYFRYLEEWGQNFCKERKKRLKQIKEECMDGSDKKYSGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSTPESGSNSDKNGATCIPPRRRRL---YVGKLEQWANKHNTETSVSQGEATEARGSEAP
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                                                                                                                                                                                                                                               EQCDRRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NTET----KKMDE------GVRTYLMKYIYKNNDIKE---
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                                                                                                                                                                                                       -NNGLAVKEANSE 318
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                                                                                                                                                                                                                                               -TSNEVSADLEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:g886376; PID:g886378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 399.5; DB 2;
Pred. No. 1.9e-19;
8; Mismatches 118;
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                                                            malaria parasite
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variant-specific surface protein - malaria parasite c; Species: Plasmodium falciparum C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #C; Accession: T14602 R; Voss, T.S.; Felger, I.; Weiss, N.; Beck, H.P. submitted to the EMBL Data Library, February 1998 A; Description: Identification of a conserved 5' flan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Geneti
A;Gene:
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A; Residues: 1-2197 <GAR>
A; Cross-references: GB:A
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.;
R;Gardner, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite F
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                      A; Molecule type: DN
A; Residues: 1-2135
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                                                                      A; Status: preliminary; translated
                                                                                         A;Accession: T14602
                                                                                                           A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          978
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                                                                                                                                                                                                                                                                                                                                                                                                         WINTKRDEFNKQSNAYSEQKKKYEEENDSAQKNNGVCGTLKDDAAEFLNRLKNGPCKNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKRTEMLGKIKEDC----YKNGGRCSGDGLKCNEIVIDKEKIFGDLLCPTCARHCRFYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPKDE-----KYQYQTAKLEDESGEKRPDSSASGTKLTDFIKRPPYFRYLEEWGENFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-MDEGVRTYLMKYIYKNNDIKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGPQNSVNDRQSLWDRIAEHVWHGMVCALTYKDDDNGLKGVVKKPQKIENPEKLWNETTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMFYTFGDYRDICLDTDISEKIADHDV-----TTAKKKITAVFQKI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRRRRLYVGGLTKLTSAGTSSESPQGGSESSRASDVSQGNGGDDITTTESLRKWFIETAA
                                                                                                                                                                                                                                                                                                                                     EENKKAEDEIDFKKPDDTFKDADNCKPCSEFKIKCENHNCSSG
                                                                                                                                                                                                                                                                                                                                                                         NSAKHARDYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                            WM-----ERWKKHYSSQKKKFQLYKNSATYNNGL--AVKEANSE---TYKNDPEVTEA
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ce: clone 3D7
                                                                                                              Z18158
                   EMBL: AF050740; NID: g2944094; PID: g2944095; PIDN: AAC05220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 398.5; DB 2; Pred. No. 1.8e-19;
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                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                       -KTQLENMICTNG
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                                                                                                                            flanking
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R.; White, O.;
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C:Accession: T14029
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rtatus: preliminary; translated
Moleculé type: mRNA;
Residues: 1-2228 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1) Reference number: Z17860; MUID:98080592; PMID:9419207
                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:AF003473; NID:g2961467; PID:g2961468; PIDN:AAC05730
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Best Local
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                      ETFFLWHRYKEEKKAVAQEGAGHGLPRVEEGSPEYDPEDK-LKEGKIPDGFLRQMFYTLG
                                                                                              VPPRRRRL---YIKKIVDWATKTESPQASGSEASSTSGSTTPPDSKEA-LLKAFVESAAI
                                                                                                                                                                    CPIVGKVLT----KDN----ESLQDACSLKYGGNNSRLGWRCVTPSGEPTTSSDKNGAIC
                                                                                                                                                                                                         CKMYQKLISEQIEKNNIHNCKKTEDA------KWKC----ENTKLGEDEG-VC
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                                                            ETFLLRQYYNSK -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKMDEGVR----TYLMKYI-----YKNNDIKE-------YLEEFASR 219
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                                                                                                                                                                                                                                                            19.6%;
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                                                                                                                                                                                                                                           Score 375; DB 2; I
Pred. No. 7.8e-18;
6; Mismatches 139;
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                                                            -NVE-----
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                                                          ---DDKILHRDMIPPEFFRSMFYTFG 116
                                                                                                                                                                                                                                                                               Length 2228
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A;Title: The large diverse gene family var encodes protein A;Reference number: Z20487; MUID:95330813; PMID:7606788
A;Accession: T28634
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Residues: 1-2182 <
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Similarity 25.4%;
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                                                                                                                              ANKNTPIEKYQYTNVKLEDESGAKSNDTIQPPTLKNFVEIPTFFRWLHEWGNSFCFERAK
                                                                                                                                                                  GVR-TYLMKYIY------
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                                                                               ELVSLKKKCDSCTLRNNGTSNKTCDDNENC--
                                                                                                                                                                                                                                          GKKVLER-----EGWWKEYGLSIWKGMLCALSY-----
                                                                                                                                                                                                                                                                                                                   TDISEKIADHDVTTAK---
                                                                                                                                                                                                                                                                                                                                                     EKKPPATQDGAGLGVSLPEPSPPGEDPQTQLQQTGVIPPDFLRQMFYTLADYKDILYSGS
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R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.
Cell 82, 77-87, 1995
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C;Species: Plasmodium falciparum
Search completed: June 20, 2003, 15:06:21 Job time: 30.6965 secs
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A;Accession: T18396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA; Residues: 1-1729 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.8
Best Local Similarity 23.6
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1
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                                                                                                                                                                                                                                                                                                                                                                                                                   TEWGEDFVKNRKKELVSLKKKCDSCTLRNN----GTSNKT------CDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.8%; Score 360.5; DB 2; 23.6%; Pred. No. 5.9e-17; tive 65; Mismatches 146;
                                                                                                                                                                                                                             ----KEANSETYKND-----PEVT--EANSAKHARDYLKTQLENMICT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SNYENEÓKDKCQTQSNN--NANEFSRT 1298
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein 'protein search, using sw model

Run on: June 20, 2003, 14:37:29; Search time 15.4461 Seconds
(without alignments)
942.514 Million cell updates/sec

Title: US-10-087-013-9
Perfect score: 1913
Sequence: 1913
Sequence: 1920SUM62
Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

30 31 32 33	222 222 223 24 25 26	11 12 13 14 15 16 17	10087654	Result No.
86 86 86 86 86 86	101.5 101.5 101.5 101.5 101.5 100.5 100.5	106.5 106.5 106.5 105.5 104.5 103.5 102.5	329 269 261 231 235 122.5 117 115 114	Score
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helicol saccha: homo sa homo sa plasmoo	Q03410 rattus norv P34111 saccharomyc Q9utk5 schizosacch P35580 homo sapien P27625 plasmodium P35749 homo sapien O51226 borrelia bu P08964 saccharomyc Q99me9 mus musculu P54100 rattus norv		9214 pla 2290 pla 0493 pla 2545 pla 0494 pla rgh4 fus 8696 dro 2380 sac 2209 mus 6495 chl	Description

98 5.1 1805 1 HMW2_MYCGE 98 5.1 2136 1 YCF2_MARPO 97.5 5.1 441 1 YYO7_METJA 97.5 5.1 5.1 5.1 1 CPT7_RANDY 97.5 5.1 726 1 HS9A_BRARE 97 5.1 726 1 YSW1_YEAST 97 5.1 807 1 YSWA_STAAU 97 5.1 976 1 SCP1_HUMAN 97 5.1 976 1 SCP1_HUMAN 97 5.1 1972 1 MYHB_MOUSE 96.5 5.0 845 1 VAV_MOUSE 96.5 5.0 845 1 VAV_MOUSE 96.5 5.0 1005 1 RASO_METJA
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HMW2_MYCGE 1 YCF2_MARPO 1 YYO7_METJA 1 CPT7_RANDY 1 CPT7_RANDY 1 HS9A_BRARE 1 YSM1_YEAST 1 HYSA_STAAU 1 SCP1_HUMAN 1 MYHB_MOUSE 1 WYHB_MOUSE 1 VAV_MOUSE 1 VAV_MOUSE 1 RASO_METJA
HAWAZ_MYCGE YCEZ_MARPO YYO7_METJA CPT7_RANDY HS9A_BRARE YSW1_YEAST HYSA_STAAU SCP1_HUMAN WYHB_MOUSE ENPL_CHICK VAV_HOUSE RASO_METJA

# ALIGNMENTS

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241 LYSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMERWKKHYSSQKKKFQLY 300	VISWVFKDKTVCKEDDIENIPQFFRWFSEWGDDYCQDKTKM	182 LSYNTETKKMDEGVRTYLMKYIYKNNDI-KEYLEEFASRPPFLRWVTEWGEDFVKNRKKE 240	562 DLSNRKL ** I	130 KIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKGMLCA 181	KNKDDKEVCKIIN	70 EAFTKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDTDISE 129	463 DKNSVDTNTKVWECKNPYILSTKDVCVPPRRQELCLGNIDRIYDKNLLMIKEHILA 518	CENTKLGEDEGVCMPPRRQNLC	Query Match 17.2%; Score 329; DB 1; Length 1435; Best Local Similarity 24.8%; Pred. No. 2.9e-15; Matches 87; Conservative 63; Mismatches 113; Indels 88; Gaps 13;	VARIANT 1031 1031 E -> TROCKIES: VARIANT 1031 1031 E -> TRAINS FCR-3 AND ITG). SEQUENCE 1435 AA; 167389 MW; 32A4309021B1C3D6 CRC64;	DOMAIN 159 1104 ESSENTIAL FOR BINDING TO	S11561; S11561.	FMBT. X57574. CABA5756 1.	an email to license@isb-sib.ch).	this statement is not removed. Usago	by non-profit institutions as long as its content is in no	tute of Bioinformatics and ics Institute. There are i	OT entry is copyright. It is produced through a		gen 175 in Plasmodium falciparum.";	conservation of a functional domain	MEDLINE=90377299; PubMed=2204835;	SPOTENOR EDON N. A	Alveolata; Apicomplexa; Hae =5835;	Erythrocyte-binding antigen EBA-175. Plasmodium falciparum (isolate Camp / Malaysia).	1-FEB-1996 (Rel. 33, Last annotation up	16, Created)	- 1	г

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DOMAIN
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: HIGH, TO P.KNOWLESI DUFFY RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-91187056; PubMed-1849231;
Fang X., Kaslow D.C., Adams J.H., Miller L.H.;
"Cloning of the Plasmodium vivax Duffy receptor.";
MOl. Biochem. Parasitol. 44:125-132(1991).

-i- FUNCTION: BINDS TO THE HUMAN ERYTHROCYTES DUFFY
                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         Malaria;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M61095; AAA63423
                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium vivax (strain Salvador I).
Eukaryota; Alveolata; Apicomplexa; Ha
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30-MAY-2000
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                                                                                                                                               84;
                                                                                                                                                          Similarity
FCKDIRWSLGDFGDIIMGTDMEGIGYSKVVENN-----LRSIF-----GTDEKAQQR
                      FFRSMFYTFGDYRDICLDTDIS----EKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLE
                                               TNLVNNTDTNFHRDITFRKLYLKRKLIYDAAVEGDLLLKLNNYRYNKD-
                                                                  TKL--NDDS---KEEDLREAFIK-----SAAAETFLLRQYYNSKNVEDDKILHRDMIPPE
                                                                                          KKTISSAIINHAFLQNTVMKNCNYKRKRRERDWDC-NTK----KDVCIPDRRYQLCMKEL
                                                                                                                QKLISEQI-----EKNNIHNC---KKTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYL
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                                                                                                                                                                                                                                                                                                                                                                         Receptor;
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(Rel. 33, Last sequence up
(Rel. 39, Last annotation
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26.2%;
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Pred. No. 3e-11;
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                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                  RECEPTOR
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lams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C.

lams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C.

coc. Natl. Acad. Sci. U.S.A. 89:7085-7089(1992).

FUNCTION: BINDS TO THE HUMAN ERYTHROCYTES DUFFY F
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MEDLINE-92357776; PubMed-1496004;

MEDLINE-92357776; PubMed-1496004;

Adams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller Padams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller Padams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller Padams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller Padams J.H., Acad. Sci. U.S.A. 89:7085-7089(1992).
                                                                                                                                                                                                           between the Swiss Institute of Bioinfor the European Bioinformatics Institute, use by non-profit institutions as long modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
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Eukaryota; Alveolata; Apicomplexa;
                   Malaria; Receptor; Glycoprotein; Signal; Multigene family.
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PIR; A35970; A35970.
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                                         SEQUENCE FROM N.A. STRAIN-ATCC 25586; MEDLINE-21886394;
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htpG (Heat shock protein htpG)
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence and analysis of the oral bacterium nucleatum strain ATCC 25566.",
J. Bacteriol. 184:2005-2018(2002).
-i- FUNCTION: Molecular chaperone. Has ATPase activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhattacharyya A., Bartman A., Gardmer W.,
Vasieva O., Chu L., Kogan Y., Chaga O., G
Larsen N., D'Souza M., Walunas T., Pusch
Fonstein M., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00298; Chaperone; ATP-bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
  Neesen J.,
"Tandemly a
                                                                                                                                                                                  Q08696;
01-FEB-1995
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY
                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
                                                                                                                               Axoneme-associated MST101(2).
                                                                                                                                                        01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                            MST2_DROHY
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                         SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=95045538; PubMed=7957199;
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  , Padmanabhan
arranged repe
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1 323 A; SUBSTRATE-BINDING (BY
324 534 B (BY SIMILARITY).
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8; Mismatches
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Pred. No. 0.
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Chaga O., Goltsman E., Bernal
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Drosophila.
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P32380;
01-OCT-1993
01-OCT-1993
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Eur. J. Biochem. 225:1089-1095(1994).
-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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lase; FBgn0020733; Dhyd\mst101(2).
m; Repeat; Multigene family; Poly
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                                        STANDARD;
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27, Created)27, Last sequence
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Pred. No. 1
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EMBL; X73297; CAA51733.1;
EMBL; U28372; AAB64791.1;
PIR; S26710; S26710
PIR; S34288; S34288.
                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92176232; PubMed=1541631;
Mirzayan C., Copeland C.S., Snyder M.;
"The NUF1 gene encodes an essential coiled-coil related
is a potential component of the yeast nucleoskeleton.";
J. Cell Biol. 116:1319-1332(1992).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.
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Johnston M., Andrews S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A spacer protein in the Saccharomyces cerew
whose transcript is cell cycle-regulated.";
J. Cell Biol. 123:1175-1184(1993).
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Kilmartin J.V., Dyos
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SUBCELLULAR LOCATION: NUCLEAR; TIGHTLY ASSOCIATED NUCLEUS. IT IS PRESENT IN A GRANULAR PATTERN THAT
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yos S.L., Kershaw D.,
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NUCLEAR LOCALIZATION SIGNAL (F

NUCLEAR LOCALIZATION SIGNAL (F
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Pred. No. 1
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SUBMILTEG (NOV-1996) to the EMBL/GenBank/DDBJ databases.

'! FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF
SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS
CHROMOSOMES DURING MEIOTIC PROPHASE.

'! SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF
SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS.

FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMIN
IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE TH
C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
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15-JUL-1998 (Rel
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ
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Submitted (APR-1995) to the
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STRAIN-Swiss; TISSUE-Testis;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=96004899; PubMed=7548215;
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                                             SYNAPTONEMAL COMPLEX (BY SIMILARITY).

DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. T. DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
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P36495; Q37303;
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15-JUL-1998 (Rel. 3
16-OCT-2001 (Rel. 4
      Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                         232.2 kDa protein (ORF1995 Chlamydomonas reinhardtii.
                             Chloroplast
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EMBL; U62862;
EMBL; U62863;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (s or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                 503 LEKEKLKNTELTASCDMLLLENKKFVQEASDMALELKKHQEDIINCKKQEERLLKQIENL
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MW: 1A4FA790D64FAFE6 CRC64;
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Boudreau E., Otis C., Turmel M.,
Boudreau E., Otis C., Turmel M.,
Boulereau E., Otis C., Turmel M.,
"Conserved gene clusters in the highly rearranged chloroplast genomes
of Chlamydomonas moewusii and chlamydomonas reinhardtii.";
Plant Mol. Biol. 24:585-602(1994).
-I- FUNCTION: ESSENTIAL FOR CELL GROWTH. MAY BE INVOLVED IN BINDING
CHLOROPLAST DNA TO EITHER THE CHLOROPLAST ENVELOPE OR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A. MEDLINE=94207185; PubMed=8155879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 44:17-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woessner J.P., Gilham N.W., Boynton J.E.; "The sequence of the chloroplast atpB gene and in Chlamydomonas reinhardtii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A large open
Chlamydomonas
                                                                                                                                                                                                                                         SEQUENCE
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MEDLINE-97218038; PubMed-9065699;
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large open reading frame (orf1995) in the chloroplast DNA of
lamydomonas reinhardtii encodes an essential protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: TO C.VULGARIS ORF819.
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S41289; S41289.
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                                                                                                      53 VHYLTKLNDDSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMF
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                                                   -YTFGDYRDICLDTDISEKIADHDVTTAK---
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein) (Meiotic synaptic protein) (Fragment).
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Q60563;
                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosome disjunction.",

J. Cell Sci. 107:2749-2760(1994).

-i- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARITY). HAVE
                                                                                                                                  or send
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Dobson M.J., Pearlman R.E., Karai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF
SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE
                                                                                                                                                                                                                                                                                                                                           SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX
                                                                                                                                                                                                                                                            FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. T DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                            DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1274
                                                                                                                                                                                                                                                                                                               SYNAPTONEMAL COMPLEX
                                                                                                                                                                                                                                                                                                                            C-TERMINUS EXTENDS WELL INTO
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                                                                                                                                  an email to license@isb-sib.ch).
                                                                                 protein;
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   553
753
                                                                  Coiled coil.
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                                                                               Meiosis;
   556
756
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Rodentia;
                                                                                 Cell
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COILED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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Sciurognathi; Muridae;
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                                                                               division;
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                                                                               Phosphorylation;
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DT 16-OCT

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Best Local S
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between
                                                                                                                                                                                                        Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volk Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister "The genome sequence of the thermoacidophilic scavenger Therm acidophilum.";
            between the Swiss Institute of Bioinformatic
the European Bioinformatics Institute. They
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                   STRAIN-DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martine
Mewes.H.-W., Frishman D., Stocker
                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
DNA double-strand break repair rad50 /
RAD50 OR TAO157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                       Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HLR8;
                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
                                                                                        SUBUNIT: Forms a com
SIMILARITY: BELONGS
                                                                                                                                         FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrel1 complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease. activity. Rad50 provides an ATP-dependent control of mrel1 by unwinding
                                                                                                                              and/or repositioning DNA
                                                                                                                  similarity)
                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation for the Swiss Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                 THEAC
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requires
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FY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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a license agreement (See http://www.isb-sib.ch/announce,
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99401 MW;
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D7F28873C824C6A8 CRC64;
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                                                                                                                                                                                                                       DNA topoisomerase
                                                                                         Tanizawa
                                                                                                                                           NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
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J. Biol. Chem. 268:25403-25400\.T. BY-1- FUNCTION: THE REACTION CATALYZED BY CONVERSION OF ONE TOPOLOGICAL ISOME
                                                                                                                                                                                                                                                                Cricetulus griseus (Chinese hamster)
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Rodentia; Sciuroo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair; Hydrolase; ATP-binding; Coiled coil; NP_BIND 30 37 ATP (BY SIMILARITY) DOMAIN 151 744 COILED COIL (POTENT
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InterPro; IPR003395; SMC_N.
Pfam; PF02463; SMC_N; 1.
                                                J. Biol. Chem. 268:25463-25468(1993)
                                                                                      "Cloning of Chinese hamster DNA tidentification of a single point
                                                                                                                                                                      MEDLINE=94064611; PubMed=8244980;
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(Rel. 30, Last sequence up
(Rel. 40, Last annotation
merase I (EC 5.99.1.2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAC11304.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GVRTYLMKYIYKNNDI----KEYLEEFASRPPFL
                                                                                                                                                  ;
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                                                                                                                                                  Kohlhagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106.5;
Pred. No. 4.
                                                                                                                                                                                                                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2C584D700CCD2CB2
                                                                                          topoisomerase mutation resp
                ISOMER
                                                                                                                                                  G.,
                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        767
                                                                                                                                                                                                                                                                                                                                                              update)
                                    TOPOISOMERASES
                                                                                                                                                    Tabuchi
                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                          responsible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158;
                DNA
                                                                                                                                                                                                                                                                    Muridae;
                                                                                                              CDNA
                TO
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                ANOTHER
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                                                                                          e for
                                                                                                                                                                                                                                                                    Cricetinae,
                                    LEADS
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                                      THE
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RESULT 14
RBP1_PLAVB
ID RBP1_P
AC Q00798
DT 01-APR
DT 01-APR
DT 01-OCT
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Best Local S
Matches 69
 Q00798;
01-APR-1993
01-APR-1993
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0416; EUTPIS SMART; SM00435; TOPEUC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001631; Topismerse_I. pfam; pf01028; Topoisomerase_I; 1. pfam; pf029219; Topoisomer_I.N; 1. prINTS; pr00416; EUTPISMRASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z21624; CAA79748.1; -.
EMBL; Z21625; CAA79748.1; -.
PIR; S32697; S32697
HSSP; P11387; 1A35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                     RBP1_PLAVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
ENZYME REGULATION: SPECIFICALLY INHIBITED BY CAMPTOTHECIN (CPT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELAX ONLY NEGATIVE SUPERCOILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLANT ALKALOID WITH ANTITUMOR ACTIVITY
                                                                                                                                                         317
                                                                                                                                                                                         286
                                                                                                                                                                                                                            281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 20.5
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00176; TOPOISOMERASE_I_EUK; e; Topoisomerase; DNA-binding. 725 DNA CLEAVA
                                                                                                                                                                                       WKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYK 321
                                                                                                                                                                                                                                                         VTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQCEKYKKWMER
                                                                                                                                                                                                                                                                                                                            KGMLCALSYNTETKKMDEGVRTY----LMKYIYKNNDIKEYL-----EEFASRPPFLR-W
                                                                                                                                                                                                                                                                                                                                                            RKLEEEEDGKLKKTKNKDKDKKGAESDNKKKKPKKEEEQKWKWWEEERYPEGIKWKFLEH
                                                                                                                                                                                                                                                                                                                                                                                              -KIADHDYTTAKKKITAVFQKIGSKTTNGKKVLERE-----GWWKE--YGLSI-W----
                                                                                                                                                                                                                                                                                                                                                                                                                                -----YFAPPKEDIKPLKRPRDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSAAAETFLLRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRDICLDT-DISE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKRKEEKIRASGDAKIKKE-----KENGFSSPPR--------IKDEPDDDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKDWRKEMTNDEKNVITNL-SKCDF--
                                                                                                                                                                                                                                                                                          KGPVFAPPY----EPLPEGVKFYYDGKVMKLSPKAEEVATFFAKMLDHEYTTKEIFRKNF
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767 AA;
(Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90867 MW;
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Pred. No. 3.8;
47; Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA CLEAVAGE (BY SIMILARITY).
S -> G (IN CPT-RESISTANT CELL).
; 347336D424EF35A9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                         TQMSQYFKDQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                164
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ENPL\_CATRO
ID ENPL\_C
AC P35016

ENPL\_CATRO P35016;

STANDARD;

PRT;

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RESULT 15

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Best Local S
Matches 85
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    merozoltes. ,
Cell 69:1213-1226(1992).
TNVOLVED IN RETICULOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M88097; AAA29743.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galinski M.R., Medina C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92315338; PubMed=1617731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium vivax (strain Belem)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reticulocyte binding protein 1 precursor RBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A reticulocyte-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                 1196
                                                                                                                                                                           1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN RETICULOCYTE CELLS.
                                                         1247
                                                                                                                                                                                                                                   1097
                                                                                                                                                                                                                                                                                           1058
                                                                                      277
                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                               17 NIHNCKK-TEDAKWKCENTKLGEDEGVCMPPRRQNLCVHYLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                               YTFGDYRDICLDTD----ISEKIADHDVTTAKKKITAVFQKIGSK-----TTNGKKV 160
                                                                                                                                                                                                                                                                                                                                                 SINNCKKYNTDIDLLRSKIKTLREEVQKEMPKRGDKCGENTTALLLKSLRDKMGKINEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Signal; Transmembrane
1 17 POTENTIAL.
                                                                                                                   SKLK-----EVINKHVSEMTQLESTAN--TLKSNAKGKENEHDLEELNKTKGQMRDIY 1246
                                                                                                                                             PFLRWVTEWGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGACKTQC----
                                                                                                                                                                          LKSV---KEV----EDKLNLVEQNEDYKKV-----
                                                                                                                                                                                                                                   NRIDEWEDIKRDVDELNVNYQVISENKVTLFKNNSVTYIEAMHSHINTVAHGITSNKNEI 1156
                                                                                                                                                                                                                                                                                           NDGRLNSLDTKKED---
                                                                                                                                                                                                                                                                                                                     ND-----DSKEEDLREAFIKSAAAETFLLRQYYNSKNVEDDKI-LHRDMIPPEFFRSMF 112
 RITVEKDKAGKVVEEMNS-----
                            ------VTEANSAKHARDYLKTQLENMI
                                                         EKLKKIAEELKE-
                                                                                   EKYKKWMERWKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKNDPE-----
                                                                                                                                                                                                     LEREGWWKEYGLSIWKGMLCALSYNTETKKMDEGVRTYLMKYIYKNNDIKEYLEEFASRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
18
2808
2827
1030
2599
2869
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2807
2826
2869
1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; B9DBE442205EBCFF
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 105.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC.
CELL ATTACHMENT SITE
CELL ATTACHMENT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENT IAL.
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                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                           -----LLKFYSESKS----KIHLSKDQKGPQ---DPL 1096
-LKTKIEKLI
                                                         -GTVNE---LKDANEKANKVEPEPERNIIGHVLE 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
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Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
 1315
                            347
                                                                                                                                                                                                                                                                                                                                                                                                            123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2869;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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01-FEB-1994
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Plant Mol. Biol. 23:583-594(1993).

-i- FUNCTION: MAY HAVE A MOLECULAR CHAPERONE ROLE IN THE PROCESSING OF SECRETED MATERIALS. IT IS PROBABLY NOT A MAJOR HEAT SHOCK RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
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-!- TISSUE SPECIFICITY: NOT DETECTED IN EXTRACTS FROM YOUNG
-UNLESS THEY ARE EXPOSED TO HEAT SHOCK FOR SEVERAL HOURS.
FOUND TO BE CONSTITUTIVELY EXPRESSED IN CELL CULTURES.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94033337: pubMed-8106014;
Schroeder G., Beck M., Eichel J., Vetter H.P., Schroeder J.;
"HSP90 homologue from Madagascar periwinkle (Catharanthus roseus):
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CARBOHYD
                                                                                                                                                                                                                                                                                                         Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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InterPro; IPR001404; Hsp90.
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                                                            400 LPPKAPQDLYESYYNS-NKSNLKLYVRRVFISDEFDE--LLPKYLNFLKGLVDS-----D
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Best Local
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(clone pS31H) ORF (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
MCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson D.S., Miller L.H., Wellems T.E.; "Isolation of multiple sequences from the Plasmodium falciparum genome that encode conserved domains homologous to those in erythrocyte-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q25989;
Q25989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 92:7100-7104(1995).
EMBL: L38454; AAC37240.1; -.
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                  679 WIDNYKKOKGRYTEVK--
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                                             WKKHYSSOKKKFOLYKNSATYNNGLAVKEANSETYKNDPEVTEANSAKHARDYLKTOLEN 345
                                                                                                            IWKGMLCALSYNT-----ET-KKMDEGVRTYLMKYIYKNNDIKEYLEEFASRDPFLRW
                                                                                                                                                                                                                                              FADYRDICLGTDISSKKDTSKGVGKVKCNIDDVFYKISN-----SIRYRKSWWETNGPV
                                                                                                                                                                                                                                                                                                                                                                                                                          CKMVQKLISEQIEKNNIHNCKKTED-AKWKCENT--KLGEDEGVCMPPRRQNLCVHYLTK
                                                                                          LTEWGENFCKEQKKEYKVLLAKCKDCDVDGDG
                                                                                                                                                                                                                                                                                  FGDYRDICLDTDI-SEKIADHDYTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYGLS
                                                                                                                                                                                                                                                                                                                            IMTNTNE--LKYAFIKCAAAETFLLWQNYKKDKNGNAEDLDEKLKGGIIPEDFKRQMFYT
                                                                                                                                                                                                                                                                                                                                                        LNDDSKEEDLREAFIKSAAAETFLLRQYY---NSKNVED-DKILHRDMIPPEFFRSMFYT
                                                                                                                                                                                                                                                                                                                                                                                                     CEIVAEMLKDKNGRTTVGECYRKETYSEWTCDESKIKMGQ-HGACIPPRRQKLCLHYLEK
                                                                                                                                                                    IWEGMLCALSYDTSLNNVNPETHKKLTEGNNNF-EKVIF-GSDSSTTLSKFSERPQFLRW
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Pred. No. 1:3e-36;
14; Mismatches 112;
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          -KIPLYKEDKDVKNSDD---ARDYLKTQLQN
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Best Local Similarity 39.4
Matches 146; Conservative
                                                                                Q95W83;
Q95W83;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                 VAR1
    Eukaryota;
                          Plasmodium
                                                             Erythrocyte
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01-JUN-2002
01-JUN-2002
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                            YSKAAGYIKKE 1648
                                                                                                                                                                                                                                                                                                   AKHARDYLKTQ 342
                                                                                                                                                                                                                                                                                                                                                                                                              WGDDFCREQKKKYNELKEKCNKCC--NNG--NVTSDECKTKCVECQKKCEEYKGFITEWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKGMLCALSY---NTETKKMDEGVRTYLMKYIYK---NNDIKEYLEBFASRPPFLRWYTE
                                                                                                                                                                                                                                                                                                                                          ENWNKQKNKYETLYTQ-
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    falciparum
Alveolata;
                                                                                (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 21,
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                                                         (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 21, Last annotation updat membrane protein 1 (Fragment).
                                                                                                                                                                PRELIMINARY;
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    Apicomplexa;
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                                                                                                                    Created)
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9; Mismatches
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  Haemosporida;
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Plasmodium
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CRC64;

isolate. intercellular

Indels Length

Gaps

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174 1426 114 1366 54

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 Pfam; PF03011; FSEQUENCE 3078
                   EMBL; L40608; AAA75396.1; -. InterPro; IPR004258; PFEMP.
                                      cytoadherence and antigenic variation infected erythrocytes.";
Cell 82:89-100(1995).
                                                                    MEDLINE=95330813; PubMed=7606788;
Su X.Z., Heatwole V.M., Warthelmer S.P., Guinet F.,
Peterson D.S., Ravetch J.A., Wellems T.E.;
"The large diverse gene family var encodes proteins
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=57267;
                                                                                                                                                   Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                          VAR-1
                                                                                                                                                                                  Variant-specific surface
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01-DEC-2001
                                                                                                                                                                                                                          Q26031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 293:2098-2100(2001).
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"Role of nonimmune IgG bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flick K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442075; PubMed=11557894;
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(TrEMBLrel. 01, Last
(TrEMBLrel. 19, Last
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Pred. No. 9.2e-35;
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 C8037C2BC3CCD7C3 CRC64;
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ion update)
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Best Local :
                           Smith J.D., Kyes S., Craig A.G., Fagan T., Hudson-Taylor D., Miller L.H., Baruch D.I., Newbold C.I.; Newlard of adhesive domains from the A4VAR plasmodium falciparum erythrocyte membrane protein-1 identifies a CD36 binding domain.";
                                                                               SEQUENCE FROM N.A. STRAIN=IT 4/25/5;
                                                                                                                                                    Miller L.H.
                                                                                                                                                                                                                                                                                                                                                                                                      026030;
                                                                                                                                                                                                                                                                                                                                                                                                               Q26030
 SEQUENCE
                   Mol. Biochem.
                                                                     MEDLINE=99094502;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
"Switches in the expression of Plasmodium falciparum correlate with changes in antigenic and cytoadherent infected erythrocytes.";
Cell 0:0-0(1995).
                                                                                                                        STRAIN-IT 4/25/5;
Smith J.D., Chitnis
                                                                                                                                                                                                                                                                                             MEDLINE=95330813; PubMed=7606788;
Su X.Z., Heatwole V.M., Wertheimer S.P.,
Peterson D.S., Ravetch J.A., Wellems T.E.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2044-2922 FROM N.A. STRAIN=IT 4/25/5; MEDLINE=95330813; PubMed=760678
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum Eukaryota; Alveolata;
                                                                                                       Smith J.D., Chitnis C.E., Craig A.G., Rober Hudson-Taylor D.E., Peterson D.S., Pinches
                                                                                                                                                                      SEQUENCE OF 2044-2922 FROM N.A.
                                                                                                                                                                                                            infected erythrocytes.";
Cell 82:89-100(1995).
                                                                                                                                                                                                                                                     "The large diverse gene family var encodes proteins cytoadherence and antigenic variation of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variant surface protein
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Local Similarity 38.8%;
nes 137; Conservative 6
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Pred. No. 1.3e
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0905M2;
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01-MAY-2000
                                                                                          Buffet P., Gamain B., Scheidig C., Baruch B., Oishi S., Fujii N Fusai T., Parzy D., Miller L.H., Gysin J., Scherf A.; "Plasmodium falciparum domain mediating adhesion to chondroitin sulfate A: A receptor for human placental infection."; Proc. Natl. Acad. Sci. U.S.A. 96:12743-12748(1999).
PRINTS; PR00284;
                  InterPro; IPR001219; Neurotoxin.
InterPro; IPR004258; PFEMP.
Pfam; PF03011; PFEMP; 1.
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                                                                                                                                                                                                                                                   MEDLINE=20006305; PubMed=10535993;
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InterPro; IPR004258; PFEMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kyes S.,
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AY-2000 (TrEMBLrel. 13,
AR-2002 (TrEMBLrel. 20,
CSA ligand (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CKMVQKLISEQIEKNNIHNCK-----KTEDAKWKCENTKLGEDEGVCMPPRRQNLCVHY
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Last sequence update)
Last annotation updat
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Pred. No. 3e
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                                                                                                                                                                                                                                                                                                                                                                             Haemosporida;
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Best Local
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Best Local Similarity
Matches 133; Conserv
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096108;
01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                              Science 282:1126-1132(1998).

EMBL; AE001366; AAC71792.1;

InterPro; IPR004258; PFEMP.

Pfam; PF03011; PFEMP; 1.

SEQUENCE 1711 AA; 196550 !
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SEQUENCE
                                                                                                                                                                                                                                                                                                       Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium".
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PfEMP1
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99021743; PubMed=9804551;
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                                                                                                                                                                     Similarity
                                                                                                       WKC---ENTKLGEDEGVCMPPRRQNLCVHYLTKLNDDSKEEDLREAFIKSAAAETFLLRQ
DVTTAKKKITAVFQKIGSKTTNGKKV-LEREGWWKEYGLSIWKGMLCALSYNTETKKMDE
                            KYKEDKQNETASTELDIDDPQTQLNGGEIPEDFKRQMFYTFGDYRDLFLGRYIG-----N
                                                                                       WRCIAPSGTTSGKDGAICVPPRTQELCLYYLKELS-DTTQKGLREAFIKTAAQETYLLWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEIWEAMLCAL-VKIGAKKDD-----FTENYGYNNVKFSDKSTTLEEFAKRPQFLRWLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYTFGDYRDFLFGTDISK--GHGEGSKLKEQIDSLFKNGDQKSPNGK---TRQEWWTEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYTFGDYRDICLDTDISEKIADHDVTTAKKKITAVFQKIGSKTTNGKKVLEREGWWKEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDNEIKKLQSQVNLKEAFIKSAAAETFFSWYYYKSKDGEGNELDKELKEGKIPPAF,LRSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLNDDSK----EEDLREAFIKSAAAETFLLRQYYNSKNVED----DKILHRDMIPPEFFRSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYDDYCYTRQKYLKDVQEKCKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGEDFVKNRKKELVSLKKKCDSCTLRNNGTSNKTCDDNENCGA-CKTQCEKYKKWMERWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSIWKGMLCALSYNTETKKMDEGVRTYLMKYIYKN---NDIKEYLEEFASRPPFLRWVTE
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3542
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                28.6%;
37.3%;
                                                                                                                                                                                                                196550 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apicomplexa; Haemosporida;
                                               -NVEDDKI-LHRDMIPPEFFRSMFYTFGDYRDICLDTDISEKIADH
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19,
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                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                     Score 547.5; DB 5
Pred. No. 1.7e-29;
3; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 550.5; DB 5
Pred. No. 2.4e-29;
8; Mismatches 115
                                                                                                                                                                                                                 7BBDE6C52742235B CRC64;
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                                                                                                                                                      105;
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                                                                                                                                                                                 <u>ن</u>
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EMBL; Y13403; CAA73831.1; JOINED.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR004258; PFEMP.
Pfam; PF03011; PFEMP; 2.
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MEDLINE=97373957; PubMed=9230440;
Rowe J.A., Moulds J.M., Newbold C.I.,
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Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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01-DEC-2001 (TrEMBLrel.
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Nature 388:292-295(1997).
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                                                                      WMERWKKHYSSQKKKFQLYKNSATYNN---GLAVKE---ANSETYKNDPE----VTEANS
                                                                                                                    FLRWFVEWYDDYCKERQKYLTEVASTCKSI----DGGQLK-CD-----RGCNNKCDEYKK
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Last annotation update)
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Q8T326;
Q8T326;
Q1-JUN-2002;
Q1-JUN-2002;
Q1-JUN-2002;
PfEMP1 (Fragn
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MEDLINE=95330813; PubMed=7606788;
Su X.Z., Heatwole V.M., Wertheimer S.P., Guinet F.,
Peterson D.S., Ravetch J.A., Wellems T.E.;
Peterson D.S., Ravetch J.A., Wellems T.E.;
"The large diverse gene family var encodes proteins"
The large diverse gene family variation of Plasmodium
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Cell 82:89-100(1995).
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NCBI_TaxID=5833;
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  (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                              HNTDTRQVDDQVKGQLFENGKNTPKNSQYQYKNVTISSVSSNGGPIGNIKLEQFASRPTF 2052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNTETKKMDEGVRTYLM------KYIYKNNDIKEY------
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                                                                                                                                                                                                                                                                                    --NCGACKTQCEKYKKWMERWKKHYSSQKKKFQLYKNSATYNNGLAVKEANSETYKN 322
                        2 (TrEMBLrel.
2 (TrEMBLrel.
2 (TrEMBLrel.
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(TrEMBLrel. 19, Last annotation updat
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                                                                                                                         PRELIMINARY;
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                        Created)
Last sequence update)
Last annotation updat
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Pred. No. 5.3e-26;
3; Mismatches 123;
                                                                                                                         PRT;
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Best Local S
Matches 113
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01-JUN-2002 (TrEMBL
01-JUN-2002 (TrEMBL
PfEMP1 (Fragment).
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                  MEDLINE-2197/235; PubMed=11930336;
Rowe J.A., Kyes S.A., Rogerson S.J., Babik
"Identification of a conserved Plasmodium
implicated in malaria in pregnancy.";
J. Infect. Dis. 185:1207-1211(2002).
EMBL; AJ420412; CAD20868.1; -.
                                                                                                                                                                                                                    Q8T325;
   SEQUENCE
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                         Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5833;
                                                                                                                                                              TM284VAR3
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Plasmodium
Eukaryota;
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J. Infect. Dis. 185:1207-1211(2002).
EMBL: AJ420411; CAD20867.1;
NON_TER 3287 3287
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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  ΑA;
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31.3%;
  188639 MW;
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Last annotation updat
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9; Mismatches
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FCA896C00B86DEA6
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                                                                                                                                 Haemosporida; Plasmodium
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odium falciparum var
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.9e-26;
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Best Local :
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Best Local :
                                                                                                                                                                                                                                 "The adhesion of Plasmodium falciparum-infected chondroitin sulfate A is mediated by P. falcipar membrane protein 1.";
                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. EMBL; AF134154; AAD29126.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9XZB8
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                   Pfam; PF03011; PFEMP;
                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Variant-specific surface protein.
                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                  Reeder J.C., Cowman A.F., Rogerson S.J., Brown G.V.,
                                                                                                                                                                                                                                                                                             MEDLINE=99238507; PubMed=10220443;
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                                                                                                                                     Similarity
                                           DOSKEEDLREAFIKSAAAETFILRQYYNSKNVEDDKILHRDMIPPEFFRSMFYTFGDYRD
                    EIRKPEDILTKFINCAAKETHFAWHKYKKDNVNAENELKSGKIPEGFRKQMYYTFGDFRD
ICLDTDISEKIADHDVT-TAKKKI--TAVFQKIGSKTTNGKKVLEREGWWKEYGLSIWKG
                                                                    CKIVDGILKGNDGSNEISGCNPKESYPDWDCKKNIDNSHSGACMPPRRQKLCVRDLTQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WMERWKKHYSSOKKKFOLYKNSATYNN----GLAVKEANSETYKNDPEVTEANSAKHARDY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKVET-DEKLREAFIQCSAAETFLLWKKYKEDNNGGEDLQNQLESGIIPDDFKRQMFYTF
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                                                                                                                                                                                              IPR004258; PFEMP.
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                                                                                                                                                                      2710 AA;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                24.18;
                                                                                                                                                                      309247 MW;
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                                                                                                                     Score 460.5;
Pred. No. 2.9e
51; Mismatches
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Pred. No. 6.2e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                097312; PRELIMINARY; 097312; 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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Nature 400:532-538(1999).
EMBL; AL034559; CAB39061.1;
Interpro; IPR004258; PFEMP.
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266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 HRSKRHTESSDSTTTSSGSVCVPPRRRKLYVGELTKWAEEARKSSTSPQPGESGVANASA
  NENCG - -
                                                                                                                                                                                                                    ISEKIKNVIEKSGDTPSRTPPGQQPSDNDPKSWWKLHAPYIWNGMIYALTYDTNTASGEK
                                                                                                                                                                                                                                         ---KKITAVFQKIG---SKTTNGKKVLERE--GWWKEYGLSIWKGMLCALSYNTET----K
                                                                                                                                                                                                                                                                                                                                                                                        PCDIVQTLF - - ESTKNLSDACGLKYGPGGKEKFPNWKCISSGSDTGSTTKQNDSEGSEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCKMVQKLISEQIEKNNIHNC-----KKTEDAKWKC-----ENTKLGEDEG----
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                                           KPTTLDSFVKRPTYFRYLEEWGETFCRERKKRLEKIKVDCEVEENTGARGGTTKQKYSGD
                                                                                                                                                                                                                                                                                                      SEEKTPQQWLQSGTIPTDflrQMfYTLGDYRDLCVGVKEDVINALKASGDNPTNKLTIQQ 1064
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                                                                                   ---YLEEFASRPPFLRWVTEWGEDFVKNRKKELVSLKKKC---DSCTLRNNGTSNKTCDD
                                                                                                                              KIEKDDAVYKKLWDEANNKPKKDNGQQDYTYEKVEIKEEDSGQKASTASQTPSPRASGEN 1184
                                                                                                                                                                                                                                                                                                                               LHRDMIPPEFFRSMFYTFGDYRDICL---DTDISEKIADHDVTTAK-----
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